

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1214	100.0	224	2	AAW51119	Human epe
2	1214	100.0	224	2	AAW06511	Human epe
3	1214	100.0	224	3	AAW94654	Human hom
4	1214	100.0	344	9	ADY18068	PRO poly
5	1000	82.4	224	2	AAW51121	Human epe
6	1000	82.4	224	3	AAW94655	Murine ho
7	993	81.8	224	2	AAW51120	Rat expend
8	490	40.4	210	6	ABR40123	Human cel
9	88	7.2	931	8	ADL72200	Mouse sal
10	84.5	7.0	211	4	AAO12630	Human pol
11	84	6.9	426	4	ABW70789	N. magada
12	83	6.8	337	6	ABU56407	Mycobacte
13	83	6.8	338	2	AAU11296	Recombina
14	83	6.8	338	2	AAW18165	Mycobacte
15	83	6.8	338	2	AAW63033	Mycobacte
16	83	6.8	338	2	AAU14852	Mycobacte
17	83	6.8	338	2	AAU14854	Antigen 8
18	83	6.8	338	4	AAW82789	Mycobacte
19	83	6.8	338	4	AAW47555	Ag85A. 12
20	83	6.8	338	5	AAW50729	Mycobacte
21	83	6.8	338	5	ABB73458	M tubercu
22	83	6.8	338	5	ABB73460	M bovis 8
23	83	6.8	338	7	AAE39295	M. tuberc

DR WPI; 1998-250952/22.

DR N-PSDB; AAV07200.

XX New isolated endymidin-like protein - used to develop products for

PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia

PT or cerebellar degeneration.

XX

PS Claim 2, 9, 10; Fig 1A-1D; 147pp; English.

XX

CC The present sequence represents the human endymidin-like protein. The

CC invention also claims for the rat endymidin-like protein (AAW51120) and

CC its corresponding cDNA (AAV07201), and the mouse endymidin-like protein

CC (AAW51121) and its corresponding cDNA (AAV07202). The endymidin-like

CC proteins of the invention are claimed to have nerve-extending activity,

CC neuro-regenerative activity in the central nervous system, gliocyte

CC stimulating activity or memory forming activity. These endymidin-like

CC proteins and the corresponding DNA sequences which encode them are also

CC claimed to be useful as therapeutic or prophylactic agents for

CC Alzheimer's disease, Parkinson's disease, Huntington's disease,

CC amyotrophic lateral sclerosis, dementia or cerebellar degeneration

XX

QQ Sequence 224 AA;

Query Match 100.0%; Score 1214; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 7.2e-124;

Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRRLPTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQPOQWEGRWYQSSG 60

DB 1 MPCRRLPTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQPOQWEGRWYQSSG 60

QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFFYLLYKDGVMFQIDQATKQCSKMLTQ 120

DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFFYLLYKDGVMFQIDQATKQCSKMLTQ 120

QY 121 PWDPLDIPQNSTFEDQYSGGQEQITVQSWDRKSARSYETWIGIYTVKDCYPVQETFT 180

DB 121 PWDPLDIPQNSTFEDQYSGGQEQITVQSWDRKSARSYETWIGIYTVKDCYPVQETFT 180

QY 181 INYSVILSTRFFDIQIGIKDPSVFTPTSTCMAQLKMSDCSW 224

DB 181 INYSVILSTRFFDIQIGIKDPSVFTPTSTCMAQLKMSDCSW 224

RESULT 2

AAV06511

ID AAV06511 standard; protein; 224 AA.

XX

AC AAV06511;

XX

DT 08-OCT-1999 (first entry)

XX

DE Human endymidin.

XX

XX Endymidin; human; Parkinson's disease; Alzheimer's disease; epilepsy;

KW amyotrophic lateral sclerosis; pain; stroke; depression; anxiety;

KW neurological disorder; psychiatric disorder; cancer; therapy; diagnosis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..37

FT Domain /note= "signal peptide"

FT /label= CD-I

FT /note= "conserved domain 1"

FT Protein 38..224

FT /note= "mature protein"

FT Domain 38..47

FT /label= CD-II

FT /note= "conserved domain 2"

FT Peptide 45..53

FT /note= "epitope"

FT Peptide 56..64

FT Domain /note= "epitope"

FT 68..77

FT /label= CD-III

FT /note= "conserved domain 3"

FT Domain 101..107

FT /label= CD-IV

FT /note= "conserved domain 4"

FT Peptide 106..114

FT /note= "epitope"

FT Domain 113..119

FT /label= CD-V

FT /note= "conserved domain 5"

FT Peptide 123..144

FT /note= "epitope"

FT Domain 125..142

FT /label= CD-VI

FT /note= "conserved domain 6"

FT Modified-site 130

FT /note= "N-glycosylated"

FT Domain 143..154

FT /label= CD-VII

FT /note= "conserved domain 7"

FT Peptide 150..160

FT /note= "epitope"

FT Domain 166..180

FT /label= CD-VIII

FT /note= "conserved domain 8"

FT Peptide 168..176

FT /note= "epitope"

FT Modified-site 182

FT /note= "N-glycosylated"

FT Domain 187..193

FT /label= CD-IX

FT /note= "conserved domain 9"

FT Peptide 196..204

FT /note= "epitope"

FT Domain 199..221

FT /label= CD-X

FT /note= "conserved domain 10"

FT Peptide 215..223

FT /note= "epitope"

XX

PN W09936565-A1.

XX

PD 22-JUL-1999.

XX

PF 13-JAN-1999; 99WO-US000818.

XX

PR 14-JAN-1998; 98US-0071330P.

PR 19-FEB-1998; 98US-0075278P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA

XX Ruben SM, Ebner R;

PI

XX WPI: 1999-458471/38.

DR N-PSDB; AAX87343.

XX

PT A novel human endymidin and related nucleic acids, useful for treating

PT and diagnosis of nervous system-related disorders.

XX

PS Claim 1; Page 76-77; 90pp; English.

XX

CC This sequence represents human endymidin, a novel member of the endymidin

CC family. It was deduced from a cDNA clone (see AAX87343) discovered in a

CC primary dendritic cell cDNA library. Additional clones have been obtained

CC from KWH2, placenta, foetal and adult liver, spinal core, osteoclastoma,

CC cerebellum, synovial fibroblast, 12-week human embryo, adrenal gland

CC tumour, whole brain, Hodgkin's lymphoma, macrophage, HEL cell and

CC chondrosarcoma cDNA libraries. Endymidin polynucleotides, polypeptides

CC (including the full-length or mature polypeptide, epitope-bearing

CC polypeptides, and modified endymidin), vectors and host cells are

CC provided, as well as methods for identifying agonists and antagonists of

CC ependymin activity. Human ependymin can be used to treat conditions in  
CC patients having need of the ependymin protein. Conditions that can be  
CC treated or detected are nervous system-related disorders, such as  
CC Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis,  
CC pain, stroke, depression, anxiety, epilepsy and other neurological or  
CC psychiatric disorders. Diagnosis of cancers of the nervous system is also  
CC included. Ependymin, or its agonists or antagonists may also be used to  
CC treat disorders of the blood-brain barrier since ependymin participates  
CC in the endothelial cell barrier by modulating cell-matrix interactions.  
CC Antagonists may inhibit formation of ependymin-collagen fibrils, which  
CC cover endothelial cells of numerous blood vessels, hence anti-ependymin  
CC antibodies may regulate angiogenesis  
XX  
XX  
SQ Sequence 224 AA;

Query Match 100.0%; Score 1214; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 7.2e-124;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRVNQSSG 60  
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRVNQSSG 60  
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120  
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120  
QY 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180  
DB 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180  
QY 181 INYSVILSTRFFDIQLGKDPSTVFTPTSTCQMAQLKMSDCSW 224  
DB 181 INYSVILSTRFFDIQLGKDPSTVFTPTSTCQMAQLKMSDCSW 224

RESULT 3  
AA94654  
ID AA94654 standard; protein; 224 AA.  
XX AA94654;  
AC  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Human homology to ependymin-like protein (HELP) amino acid sequence.  
XX  
KW Homology to ependymin-like protein; HELP; chromosome 7p14-12;  
KW central nervous system disorder; peripheral nervous system disorder;  
KW Alzheimer's disease; memory loss; stroke; neuronal damage;  
KW osteoblast differentiation; proliferation; stimulation; bone wear;  
KW arthritis; osteoporosis; cerebral cavernous malformation;  
KW Charcot-Marie-Tooth syndrome; human; netrin like protein; NEL.  
XX

OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..37  
FT /label= Putative signal peptide  
FT Protein 38..224  
FT /label= Homology to ependymin-like protein  
XX  
XX WO200032746-A2.  
PN  
XX  
XX 08-JUN-2000.  
XX  
XX 30-NOV-1999; 99WO-US028341.  
XX  
XX 30-NOV-1998; 98US-00201442.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX  
PI Pan Y;

DR WPI; 2000-412299/35.  
DR N-PSDB; AAA27982.  
XX  
PT New nucleic acid molecules, designated NEL, useful for treating  
PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and  
PT neuronal damage (e.g. stroke).  
XX  
PS Claim 9; Fig 4; 97pp; English.  
XX  
CC This sequence represents a human homology to ependymin-like protein  
CC (HELP) amino acid sequence. Ependymin is a protein that is involved in  
CC memory and neuronal regeneration. The human HELP gene is located on  
CC chromosome 7p14-12. Northern analysis of HELP expression showed that an  
CC approximately 3kb HELP transcript is expressed in the brain, heart, and  
CC skeletal muscle. HELP is a secreted protein. Modulators of HELP  
CC expression or activity can be used to treat disorders of the central  
CC nervous system or peripheral nervous system, e.g. neuronal disorders,  
CC memory associated disorders, such as Alzheimer's disease or stroke, or to  
CC treat neuronal damage. HELP polypeptides, nucleic acids and modulators of  
CC HELP expression or activity may be useful for modulation of osteoblast  
CC differentiation, stimulation or proliferation. They may also be used to  
CC treat cartilage or bone wearing, arthritis or osteoporosis, disorders  
CC such as cerebral cavernous malformation and Charcot-Marie-Tooth disease.  
CC The present invention also relates to a secreted protein with homology to  
CC netrin, called netrin like protein or NEL. NEL is also referred to as  
CC TANGO 205 or T205. Netrin is a chemoattractant. Biological activities of  
CC NEL include interaction with the protein encoded by deleted in colorectal  
CC cancer, modulation of axon growth, migration and development, modulation  
CC of development of the nervous system, and modulation of the guidance of  
CC central nervous system commissural axons and peripheral motor axons  
XX  
XX SQ Sequence 224 AA;

Query Match 100.0%; Score 1214; DB 3; Length 224;  
Best Local Similarity 100.0%; Pred. No. 7.2e-124;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRVNQSSG 60  
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRVNQSSG 60  
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120  
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120  
QY 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180  
DB 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180  
QY 181 INYSVILSTRFFDIQLGKDPSTVFTPTSTCQMAQLKMSDCSW 224  
DB 181 INYSVILSTRFFDIQLGKDPSTVFTPTSTCQMAQLKMSDCSW 224

RESULT 4  
ADY18068  
ID ADY18068 standard; protein; 344 AA.  
XX  
AC ADY18068;  
XX  
XX 05-MAY-2005 (first entry)  
XX  
XX PRO polypeptide SEQ ID NO 3874.  
XX  
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; diagnosis.  
XX  
OS Homo sapiens.  
XX  
XX WO2005016962-A2.  
PN







Db 4 RAPPRLVQGGRETWLGLGGLWMTLCGLGMAGSPGTFQPCAPQWEGRQVLYQQSSGHS 63  
QY 64 RALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPWD 123  
Db 64 RALVSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKCAKIPLAEPWD 123  
QY 124 PLDIPONSTFEDQYSIGGPOEQITVQEWSDRKSARSYETWIGIYTVKDCYVQVQETTTNY 183  
Db 124 PLDIPONSTFEDQYSIGGPOEQIMVQEWSDRRTARSYETWIGVYTAQDCYVQVQETIRNY 183  
QY 184 SVTLSTRFFEDIQIGKIDPSVFTPPSTCOMAQLEKMSDSCS 223  
Db 184 TVVLSTRFFEDVQIGKIDPSVFTPPSTCQTAQPERMKENCSS 223

RESULT 8  
ABR40123  
ID ABR40123 standard; protein; 210 AA.

XX ABR40123;  
XX 04-JUL-2003 (first entry)  
XX Human cell adhesion and extracellular matrix protein, CADECM-20.  
XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;  
KW anticonvulsant; neurotropic; neuroprotective; immunosuppressive;  
KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;  
KW gene therapy; cell adhesion; extracellular matrix; CADSCM;  
KW immune system disorder; AIDS; allergy; neurological disorder; stroke;  
KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;  
KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;  
KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;  
KW atherosclerosis.  
XX Homo sapiens.  
XX OS

XX WO2003027230-A2.  
XX 03-APR-2003.  
XX 02-AUG-2002; 2002WO-US024649.  
XX 03-AUG-2001; 2001US-0309964P.  
PR 03-AUG-2001; 2001US-0310119P.  
PR 17-AUG-2001; 2001US-0313091P.  
PR 31-AUG-2001; 2001US-0316771P.  
PR 07-SEP-2001; 2001US-0317896P.  
PR 21-SEP-2001; 2001US-0324781P.  
PR 05-OCT-2001; 2001US-0327606P.  
PR 12-OCT-2001; 2001US-0328960P.  
PR 09-NOV-2001; 2001US-0344471P.  
PR 17-MAY-2002; 2002US-0381291P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;  
PI Forsythe IJ, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;  
PI Kallick DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;  
PI Wallia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;  
XX WPI; 2003-354645/33.  
DR N-PSDB; ACC00411.  
XX New human cell adhesion and extracellular matrix proteins (CADECM),  
PT useful for diagnosing, treating or preventing disorders associated with  
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies  
PT or stroke.  
XX Claim 1; Page 203; 234pp; English.  
XX The present invention relates to novel human cell adhesion and

CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding  
CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences  
CC and proteins are useful in diagnosing, treating and preventing disorders  
CC associated with aberrant expression of CADECM, such as immune system  
CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,  
CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's  
CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic  
CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell  
CC proliferative disorders (e.g. cancer or atherosclerosis)  
XX Sequence 210 AA;  
Query Match 40.4%; Score 490; DB 6; Length 210;  
Best Local Similarity 100.0%; Pred. No. 1.1e-44;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFGRAPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRCPQAPQWEGRQVLYQQSSG 60  
Db 121 MFGRAPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRCPQAPQWEGRQVLYQQSSG 180  
QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKR 90  
Db 181 RNSRALLSYDGLNQRVRVLDERKALIPCKR 210  
RESULT 9  
ADL72200  
ID ADL72200 standard; protein; 931 AA.  
XX ADL72200;  
XX 20-MAY-2004 (first entry)  
XX Mouse salt-inducible kinase 2 (SIK2) enzyme.  
XX SIK2; salt-inducible kinase 2; cAMP; antidiabetic; anorectic;  
KW hypotensive; antiarteriosclerotic; mouse; enzyme.  
XX Mus musculus.  
XX WO2004018669-A1.  
XX 04-MAR-2004.  
XX 20-AUG-2003; 2003WO-JP010535.  
XX 21-AUG-2002; 2002JP-00240092.  
PR 31-JAN-2003; 2003JP-00023295.  
XX (PROT-) PROTEIN EXPRESS CO LTD.  
PA (TAKE/) TAKEMORI H.  
PA (OKAM/) OKAMOTO M.  
XX Takemori H, Okamoto M;  
XX WPI; 2004-238976/22.  
DR N-PSDB; ADL72199.  
XX Salt inducible kinases 2 and antibodies against them for treatment of  
PT diabetes, obesity, hypertension, arteriosclerosis, circulatory disorders.  
XX Claim 1; SEQ ID NO 2; 133pp; Japanese.  
XX The invention relates to salt-inducible kinase (SIK) 2 polypeptides and  
CC encoding polynucleotides that may control the translation activity of a  
CC gene under the control of a cAMP response sequence. The SIK2 polypeptides  
CC and polynucleotides may be used in medical compositions for treating and  
CC detecting diabetes, obesity, hypertension, arteriosclerosis, circulatory  
CC disorders and high uric acid levels in the blood. The present sequence  
CC represents a mouse salt-inducible kinase 2 polypeptide.  
XX Sequence 931 AA;  
SQ



CC magadii, for production of proteins and other polymers (e.g.  
CC poly(hydroxybutyrate)). Vectors containing (I) allow controlled,  
CC inducible expression of compounds in Archaea. (Updated on 06-AUG-2003 to  
CC correct OS field.)

XX  
SQ Sequence 426 AA;

Query Match 6.9%; Score 84; DB 4; Length 426;

Best Local Similarity 23.3%; Pred. No. 8.6;

Matches 42; Conservative 29; Mismatches 80; Indels 30; Gaps 9;

QY 48 WEGQVMYQSSGRNSRALLSYDGLNQRVVLDERKALIPCKLFEYILLYKDGWVFQID 107

DB 192 WASDEDMGIANGVN---VDDYDSVDEAMDVAHEVAGYVPSGLMMIVDASDD-----D 242

QY 108 QATKQCKMTLTQPW-DPL--DIPONSTFEDQYSIGPQEQITVQEWSDRKSARSYETWI 164

DB 243 LAAYQLGKFAVSEFWYNPLWNEIPAGETVSK--NVGDPEQGTFFEGGDEAGGPGVNVLI 300

QY 165 GIYTVKDCVPVQETFTINYSVILSTRFFDIQLGKIDPSVFTPESTCQMAQLE----KMSE 220

DB 301 ---DVS DANRVSNVAVT--TAGADSDTSFFDIRR-----TKVYTAEMLELDLESLOVSD 348

QY 221 D 221

DB 349 D 349

RESULT 12

ABU56407

ID ABU56407 standard; protein; 337 AA.

AC

AC ABU56407;

XX

XX 31-MAR-2003 (first entry)

XX Mycobacterium tuberculosis 32kDa protein.

DE Antibacterial; tuberculosis; vaccine; gene therapy; 32kDa protein.

XX

XX Mycobacterium tuberculosis.

OS

FN US2002131975-A1.

XX

XX 19-SEP-2002.

XX

XX 14-SEP-2001; 2001US-00953510.

XX

XX 23-NOV-1993; 93US-00156358.

XX 12-AUG-1994; 94US-00289667.

XX 23-MAY-1995; 95US-00447398.

XX 31-OCT-1995; 95US-00551149.

XX 06-DEC-1995; 95US-00568357.

XX 23-MAY-1996; 96US-00652842.

XX 21-SEP-1998; 98US-00157689.

XX (REGC ) UNIV CALIFORNIA.

PA Horwitz MA, Harth G;

PI

XX WPI; 2003-174073/17.

XX N-PSDB; ABX75989.

XX

XX New vaccine, useful for promoting an immune response against infectious

XX pathogens of the genus Mycobacterium in a mammalian host.

XX Example 1; Page 15-16; 82pp; English.

XX

XX The invention describes a vaccine for promoting an immune response, in a  
XX mammalian host, against infectious pathogens of the genus Mycobacterium,  
XX comprising at least 1 immunodominant epitope of at least one majority  
XX abundant extracellular product comprising Mycobacterium tuberculosis 110,  
XX 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14, 12 kD protein or

CC their analogues, homologues or subunits. The proteins and polypeptides of  
CC the invention are useful in gene therapy and treatment of diseases caused  
CC by Mycobacterium such as tuberculosis. This is the amino acid sequence of  
CC the Mycobacterium tuberculosis 32kDa protein

XX  
SQ Sequence 337 AA;

Query Match 6.8%; Score 83; DB 6; Length 337;

Best Local Similarity 40.0%; Pred. No. 7.8;

Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;

QY 8 RTVPGALGAWLLGGLWANTLGLCSLGAVGAP----RPGCAPQOWGROVMYQ-QSSGRN 62

DB 17 RLTVGVAGAAALVSGL-VGAVGGTATAGAFSRPGLPVEYLQVPSMGRDIKVFQSGGAN 75

QY 63 SRALLSYDGL 72

DB 76 SPALYLLDGL 85

RESULT 13

AAR11296

ID AAR11296 standard; protein; 338 AA.

XX

XX AAR11296;

XX

XX 25-MAR-2003 (revised)

DT 30-MAY-1991 (first entry)

XX Recombinant M.tuberculosis 32kD antigen.

DE tuberculosis; vaccine; BCG; antigen.

XX

XX Mycobacterium tuberculosis.

OS

XX Key

XX Location/Qualifiers

FT Peptide

FT 1..43

FT /label= signal peptide

FT 44..338

FT /label= tuberculosis 32kD antigen

XX

XX EP419355-A.

XX

XX 27-MAR-1991.

XX

XX 19-SEP-1990; 90EP-00402590.

XX

XX 19-SEP-1989; 89EP-00402571.

XX (INNO-) INNOGENETICS NV SA.

XX Content J, Dewit L, Debruyne J, Vanvooren JP;

XX WPI; 1991-088933/13.

XX N-PSDB; AAQ11082.

XX

XX Polypeptide comprising recombinant polypeptide - with defined peptide

XX sequence(s) used for diagnosis and for preparing vaccine against

XX tuberculosis.

XX Claim 3; Fig 5; 134pp; English.

XX

XX Polyclonal antiserum was raised in rabbits to the 32kD protein of M.

XX bovis BCG. The antiserum was then used to screen a lambda gt11

XX recombinant DNA library constructed from genomic DNA of M. tuberculosis

XX (Erdman strain). Positive clones were analysed and sequenced. The deduced

XX amino-terminal amino acid sequence of the mature protein corresponds to

XX the same amino acid sequence of the MPB 59 antigen except for 3 amino

XX acid differences. Recombinant polypeptides of the invention contain at

XX least one sequence selected from the following (numbering refers to amino

XX acid position 1 as -43, etc.): -30 to -1, 12 to 31, 36 to 55, 77 to 96,

XX 101 to 120, 175 to 194, 211 to 230 and 275 to 295. See also AAQ11081,

XX AAQ11083, AAQ11086-90, AAQ11101-8, AAR11297-R11304. (Updated on 25-MAR-

CC 2003 to correct PI field.)  
XX  
SQ Sequence 338 AA;  
  
Query Match 6.8%; Score 83; DB 2; Length 338;  
Best Local Similarity 40.0%; Pred. No. 7.9;  
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;  
  
QY 8 RTVPGLGAWLLGGLMAWTLCGLCSLGAAGAP---RPCOAPQOWEGROVMYQ-QSSGRN 62  
DB 17 RLTVGAVGAALVSGL-VGAVGGTATAGAFRRPGLPVEYLQVPSMGRDIKVFQSGGAN 75  
  
QY 63 SRALLSYDGL 72  
DB 76 SPALYLLDGL 85  
  
RESULT 14  
AAW18165  
ID AAW18165 standard; protein; 338 AA.  
XX  
AC AAW18165;  
XX  
DT 13-AUG-1997 (first entry)  
XX  
DE Mycobacterium tuberculosis extracellular 32AKD protein.  
XX  
KW Vaccine; vaccinating agent; M.tuberculosis; pathogen; bacteria; virus;  
XX fungus; protozoan; HIV.  
XX  
OS Mycobacterium tuberculosis.  
XX  
FH Key Location/Qualifiers  
FT Protein 44..338  
FT /label= Mature  
XX  
PN WO9637219-A1.  
XX  
PD 28-NOV-1996.  
XX  
PF 23-MAY-1996; 96WO-US007781.  
XX  
PR 23-MAY-1995; 95US-00447398.  
PR 20-OCT-1995; 95US-00545926.  
PR 31-OCT-1995; 95US-00551149.  
PR 06-DEC-1995; 95US-00568357.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Horwitz MA, Harth G;  
XX  
WPI; 1997-020936/02.  
DR N-PSDB; AAT71599.  
XX  
XX  
PT Vaccines derived from M.tuberculosis major abundant extracellular  
PT proteins - are easy to prepare and less toxic than conventional killed or  
PT attenuated vaccines, useful for protecting against or treating  
PT Mycobacterial infections.  
XX  
XX  
PS Claim 1; Page 36-38; 193pp; English.  
XX  
XX  
CC A vaccinating agent for promoting an immune response in a mammal against  
CC Mycobacterium pathogens comprises at least one majorly abundant  
CC extracellular protein, i.e. the M.tuberculosis 110, 80, 71, 58, 45, 32A,  
CC 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins, or their analogues,  
CC homologues and subunits. The present sequence represents the 32A kD  
CC protein. The vaccinating agents are used to protect against (or to treat  
CC existing) infections by Mycobacterium (especially M. tuberculosis) while  
CC the epitopes can also be used to detect presence of an immune response to  
CC a Mycobacterium pathogen. The vectors, containing the DNA for the  
CC extracellular proteins, are used to transform cells for production of  
CC recombinant DNA molecules. More generally the DNA from other pathogens  
CC can be used in vaccines, e.g. against other bacteria, viruses, fungi and

CC protozoa. Since different combinations of DNA can be used, a wide range  
CC of effective compositions can be produced. They generate a response  
CC against the antigens most often found on infected cells during the  
CC infection, regardless of the strength or specificity of the immune  
CC response. The vaccines are easy to produce and less toxic than known  
CC killed or attenuated vaccines, so can be given to immunocompromised  
CC subjects, e.g. those with HIV infection  
XX  
SQ Sequence 338 AA;  
  
Query Match 6.8%; Score 83; DB 2; Length 338;  
Best Local Similarity 40.0%; Pred. No. 7.9;  
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;  
  
QY 8 RTVPGLGAWLLGGLMAWTLCGLCSLGAAGAP---RPCOAPQOWEGROVMYQ-QSSGRN 62  
DB 17 RLTVGAVGAALVSGL-VGAVGGTATAGAFRRPGLPVEYLQVPSMGRDIKVFQSGGAN 75  
  
QY 63 SRALLSYDGL 72  
DB 76 SPALYLLDGL 85  
  
RESULT 15  
AAW63033  
ID AAW63033 standard; protein; 338 AA.  
XX  
AC AAW63033;  
XX  
DT 23-OCT-1998 (first entry)  
XX  
DE Mycobacterium tuberculosis 32 kD protein sequence.  
XX  
KW Mycobacterium tuberculosis; vaccination; extracellular product;  
XX immunodominant epitope; interleukin-12; MF59; immune response;  
XX opsonising humoral response; intracellular pathogen.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO9831388-A1.  
XX  
PD 23-JUL-1998.  
XX  
PF 15-JAN-1998; 98WO-US000942.  
XX  
PR 21-JAN-1997; 97US-00786533.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Horwitz MA, Harth G, Lee B;  
XX  
WPI; 1998-413815/35.  
DR N-PSDB; AAW42596.  
XX  
XX  
PT Vaccines against Mycobacterium containing major extracellular proteins -  
PT used to, e.g. induce protective and therapeutic immune responses, and for  
PT detecting an immune response.  
XX  
XX  
PS Example 2; Page 38-40; 236pp; English.  
XX  
XX  
CC This represents a Mycobacterium tuberculosis 32 kD protein. The invention  
CC provides an agent for vaccinating mammals against Mycobacterium. The  
CC agent comprises at least one of the major abundant extracellular 110, 80,  
CC 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M.  
CC tuberculosis, or at least 1 of their immunodominant epitopes and  
CC interleukin-12 (IL-12) or MF59 as adjuvants. The agent containing the  
CC nucleic acid encoding the extracellular products are used to raise a  
CC protective or therapeutic immune response against Mycobacterium,  
CC specifically M. tuberculosis. The immunodominant epitopes can also be  
CC used (typically in a cutaneous hypersensitivity test) to detect an immune  
CC response to vaccination. Preparation of the agent does not require  
CC selection of the most immunogenic products, so large scale production and  
CC purification are easy, resulting in a consistent, standardised

CC formulation, having lower toxicity than killed or attenuated vaccines.  
CC The agents provide a rapid and effective response (including a strong  
CC cell-mediated component) and are safe even in immunocompromised subjects.  
CC They prevent development of an opsonising humoral response that might  
CC spread intracellular pathogens  
XX  
SQ Sequence 338 AA;

Query Match 6.8%; Score 83; DB 2; Length 338;  
Best Local Similarity 40.0%; Pred. No. 7.9;  
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;  
QY 8 RTVPGALGAWLLGGLWLTLCGLCSLGVAVGAP-----RPCQAPQOWEGRQVWYQ-QSSGRN 62  
DB 17 RLVVGVAVGAALVSGL-VGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGAN 75  
QY 63 SRALLSYDGL 72  
DB 76 SPALYLLDGL 85

Search completed: June 10, 2006, 02:51:52  
Job time : 205 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model  
Run on: June 10, 2006, 02:52:09 ; Search time 41 Seconds  
(without alignments)  
525.672 Million cell updates/sec

Title: US-10-733-646-2  
Perfect score: 1214  
Sequence: 1 MPCRPLRTVPGALGALLG.....TPPSTCQMAQLEKMSDECSW 224

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	192.5	15.9	221	2 JC1251	ependymin Om-II pr
2	190.5	15.7	221	2 JC1250	ependymin Om-I pre
3	185.5	15.3	221	2 I50538	ependymin - northe
4	167.5	13.8	215	2 I51377	ependymin precurs
5	163.5	13.5	212	2 I50490	ependymin - Atlant
6	156.5	12.9	216	2 J10090	ependymin precurs
7	154.5	12.7	217	2 A43820	ependymin precurs
8	153.5	12.6	216	2 A32636	ependymin II precu
9	87	7.2	1085	2 E70834	probable regulator
10	84	6.9	845	2 S75644	hypothetical prote
11	83	6.8	338	2 S10326	alpha-antigen A, e
12	83	6.8	338	2 H70857	32K antigen fbpA p
13	82.5	6.8	493	2 AB2434	hypothetical prote
14	80.5	6.6	957	2 T15976	hypothetical prote
15	79.5	6.5	2548	2 E59435	myosin IXA (import
16	79	6.5	257	2 C97109	specialized DNA-de
17	79	6.5	257	2 I40621	probable transcrip
18	78.5	6.5	275	2 A72319	conserved hypothet
19	78.5	6.5	1541	2 S46686	hypothetical prote
20	78	6.4	288	2 I55184	repA protein - Esc
21	78	6.4	373	2 T12063	xpsL protein - Xan
22	77.5	6.4	381	2 C86358	Similar to zinc fi
23	77.5	6.4	552	2 S50313	iron transport pro
24	77.5	6.4	643	2 G64412	hypothetical prote
25	77	6.3	678	2 T05821	hypothetical prote
26	76.5	6.3	323	2 A32348	alpha-antigen B pr
27	76.5	6.3	325	2 S29663	antigen 85-B precu
28	76	6.3	295	2 T40061	hypothetical prote
29	76	6.3	325	2 A37185	alpha-antigen prec

30	76	6.3	1118	1 A49724	protein-tyrosine-p
31	75.5	6.2	600	2 H81733	DNA primase TC0175
32	75.5	6.2	686	1 E64946	oligopeptidase B (
33	75	6.2	747	1 WZBE45	gene 45 protein -
34	75	6.2	1148	2 T13347	Cnn protein - frui
35	74.5	6.1	615	2 PH0853	methyl-directed mi
36	74.5	6.1	632	2 S64786	hypothetical prote
37	74	6.1	1456	1 A36563	mannose receptor p
38	73.5	6.1	327	2 S20038	fibronectin-bindin
39	73.5	6.1	327	2 G87162	antigen 85A, mycol
40	73.5	6.1	1219	2 S54570	probable membrane
41	73.5	6.1	1720	2 T07258	cell division prot
42	73	6.0	327	1 JQ0965	chitinase (EC 3.2.
43	73	6.0	440	2 T32457	hypothetical prote
44	73	6.0	1451	2 B86286	F9L1.15 protein -
45	73	6.0	1641	2 T10955	early nodulin bind

ALIGNMENTS

RESULT 1

JC1251  
ependymin Om-II precursor - rainbow trout  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: JC1251  
R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.  
Gene 118, 189-196, 1992  
A:Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and  
A:Reference number: JC1250; MUID:92380503; PMID:1511892  
A:Accession: JC1251  
A:Molecule type: mRNA  
A:Residues: 1-221 <MUE>  
A:Cross-references: UNIPROT:P28771; UNIPARC:UPI000012A096; GB:M93698; NID:g213413; PID:  
C:Comment: This protein shares several characteristics with soluble glycoproteins medi  
C:Genetics:  
A:Gene: Om-II  
C:Superfamily: ependymin  
C:Keywords: Glycoprotein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-221/Product: ependymin Om-II #status predicted <MAT>  
F:33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	15.9%	Score	192.5	DB	2	Length	221
Best Local Similarity	25.0%	Pred. No.	8e-11				
Matches	49	Conservative	39	Mismatches	103	Indels	5
Gaps	3						
QY	25	WTLGCLGSLGAVGAPRPCQAPQWEGRQVMYQQSSGRNSRALLSYDGLNQVRVLDERKA	84				
Db	12	WLCIGATALAESHCPOHCTSPNMTGVLTVMALTGGEIKATCHYSYDSINKLRFTESEMH	71				
QY	85	LIPCKRLFEVILYKGMFQIDQATKQCSKMTUTQPDPLDIPONSTFEDQSYSGG---	141				
Db	72	LNNKTEHLEDYLMPEEGVFYDIDMKQSCCKMSLHSHAHLELPAGAHHQVELFLGSDTV	131				
QY	142	PQSQITVQWSDRSARSYETWIGIYTVKQCPVQETFTINYSVILSTRFRFDIQLGDKDP	201				
Db	132	QEDNIKVINWVG-SVAETKQGYSAITTVGCLPL-STFYSTDSTITLLFSNSEVTEVKAP	189				
QY	202	SVFTPPSTCQMAQLEK	217				
Db	190	EMTLPSCFAVELEE	205				

RESULT 2

JC1250  
ependymin Om-I precursor - rainbow trout  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: JC1250; PC1124  
R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.  
Gene 118, 189-196, 1992

A;Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and m  
A;Reference number: JCI250; MUID:92380503; PMID:1511892  
A;Accession: JCI250  
A;Molecule type: mRNA  
A;Residues: 1-221 <MUE>  
A;Cross-references: UNIPROT:P28770; UNIPARC:UPI000012A092; GB:M93697; NID:g213411; PIDN:  
A;Accession: PC1124  
A;Molecule type: protein  
A;Residues: 22-44;198-221 <MU2>  
A;Cross-references: UNIPARC:UPI00001788FF; UNIPARC:UPI0000178900  
C;Comment: This protein shares several characteristics with soluble glycoproteins mediab  
C;Genetics:  
A;Gene: Om-1  
C;Superfamily: ependymin  
C;Keywords: glycoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-221/Product: ependymin Om-1 #status experimental <MAT>  
F;33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 15.7%; Score 190.5; DB 2; Length 221;  
Best Local Similarity 24.0%; Pred. No. 1.2e-10;  
Matches 50; Conservative 42; Mismatches 111; Indels 5; Gaps 3;  
QY 16 AWLLGLWATLCLGCLGAVGAPRCPQAPQWEGRQVMYQSSGRNSRALLSYDGLNQR 75  
DB 3 AFVAALSIWLCUGATTLAESHGPHQCTSPNMTGVLTVLALTGGEIKATGHYSYDSTDKK 62  
QY 76 VRVLDERKALIPCKRLFEYLLYKDGVMFOIDQATKQCKMTLTQPDPLDIPQNSTFFED 135  
DB 63 IRTESEMHNLKTEHLEDYLMLEEGVFYDIDMKQSKCKMSLASHAHLELPAGAAHQV 122  
QY 136 QYSIGG---PQEQITVOEWSDRKSARSYETWIGIYTKDCYPVOETFTINYSVLSTRFF 192  
DB 123 ELFLGSDTVOEEDIKNVIWTSVPETKQGYFLST-ITVGECLPL-STFYSTDSITLLFSNS 180  
QY 193 DIQLGKIDPSVFTPPSTCQMAQLEKMS 220  
DB 181 EVVTEKRAPEVFNLPFCGVELEEAPE 208  
RESULT 3  
150538  
ependymin - northern pike  
C;Species: Esox lucius (northern pike)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50538  
R;Mueller-Schmid, A.; Gansse, B.; Gorr, T.; Hoffmann, W.  
J. Mol. Evol. 36, 578-585, 1993  
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Clu  
A;Reference number: I50490; MUID:93353529; PMID:8350351  
A;Accession: I50538  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-221 <MUE>  
A;Cross-references: UNIPROT:P32188; UNIPARC:UPI000012A09D; GB:L09066; NID:g305096; PIDN:  
C;Genetics:  
A;Gene: Epd  
C;Superfamily: ependymin  
C;Keywords: glycoprotein  
F;37,77,101/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 15.3%; Score 185.5; DB 2; Length 221;  
Best Local Similarity 27.3%; Pred. No. 3.7e-10;  
Matches 59; Conservative 34; Mismatches 106; Indels 17; Gaps 6;  
QY 13 ALGAWLLGGIWAATLCLGCLGAVGAPRCPQAPQWEGRQVMYQSSGRNSRALLSYDGL 72  
DB 8 ALSIWLC--LGATTLAE--SLAQSHGPHQCTSPNMTGVLTVMALNGEIKATGHYHYDTT 63  
QY 73 NQRVVRVLDERKALIPCKRLFEYLLYKDGVMFOIDQATKQCKMTLTQPDPLDIPQNST 132  
DB 64 DKKLRTFESMHLNKSEHLEDYLMLEEGVFYDIDLNQSKCRKMSLQSHAHLELPAGAV 123

QY 133 FEDQYSIGG---PQEQITVOEW-----SDRKSARSYETWIGIYTKDCYPVOETFTINYSV 185  
DB 124 HQVELFLGSDTVOEENIKVINWMSVPETKQGYSVST-----TVGDCPLP-STFYSTDSI 177  
QY 186 ILSTRFFDIQLGKIDPSVFTPPSTCQMAQLEKMSD 221  
DB 178 TLLPNSQVTVTEKPEVEFSLPSFCGEGLEEDTHND 213  
RESULT 4  
151377  
ependymin precursor - common carp  
C;Species: Cyprinus carpio (common carp)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I51377  
R;Adams, D.S.; Shashoua, V.E.  
Gene 141, 237-241, 1994  
A;Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.  
A;Reference number: I51377; MUID:94215910; PMID:8163195  
A;Accession: I51377  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-215 <ADA>  
A;Cross-references: UNIPROT:P38528; UNIPARC:UPI000012A09B; EMBL:U00432; NID:g397655; PI  
C;Genetics:  
A;Gene: epn  
A;Introns: 28/1; 39/3; 84/3; 147/1; 175/2  
C;Superfamily: ependymin  
Query Match 13.8%; Score 167.5; DB 2; Length 215;  
Best Local Similarity 24.4%; Pred. No. 1.9e-08;  
Matches 50; Conservative 47; Mismatches 89; Indels 19; Gaps 8;  
QY 30 LCSLGAVGAPR-PCQAPQWEGRQVMYQSSGRNSRAL--LSYDGLNQRVVRVLDERKALI 86  
DB 14 LCVAWASSNRQPCCHSPPLTSG--TMKVYSTGHDLASGEFSYDSKANKRPFVEDTAHAN 71  
QY 87 PKRLFEYLLYKDGVMFOIDQATKQCKMTLTQPDPLDIPQNSTFEDQYSIGGP---Q 143  
DB 72 KTHM-DVLVHFEEGVLVEIDSKNESCKKETLQFRKHLMEIPPDATHESEIYNGSPSITE 130  
QY 144 EOITVOEWSDR---KSARSYETWIGIYTKDCYPVOETFTINYSVLSTRFFDIQLGK 199  
DB 131 QGLRVVRWNGKLPDLHAHYSLSLT-----TSCGCLPVSGSYGDKKLLFS-PFGVETVD 184  
QY 200 DPSVFTPPSTCQMAQLEKMSDPCSW 224  
DB 185 DQQVFVPPAYCEAFAFEAPDDHSF 209  
RESULT 5  
150490  
ependymin - Atlantic herring  
C;Species: Clupea harengus, Clupea harengus harengus (Atlantic herring)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50490  
R;Mueller-Schmid, A.; Gansse, B.; Gorr, T.; Hoffmann, W.  
J. Mol. Evol. 36, 578-585, 1993  
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Cl  
A;Reference number: I50490; MUID:93353529; PMID:8350351  
A;Accession: I50490  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-212 <MUE>  
A;Cross-references: UNIPROT:P32187; UNIPARC:UPI000012A09A; GB:L09065; NID:g304576; PIDN:  
C;Genetics:  
A;Gene: Epd  
C;Superfamily: ependymin  
C;Keywords: glycoprotein  
F;69,92,112/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 13.5%; Score 163.5; DB 2; Length 212;  
Best Local Similarity 24.8%; Pred. No. 4.5e-08;





Query Match 12.6%; Score 153.5; DB 2; Length 216;  
Best Local Similarity 23.3%; Pred. No. 4.1e-07;  
Matches 48; Conservative 45; Mismatches 97; Indels 11; Gaps 7;

QY 30 LCSGLGAVGAPR-PCQAPQWEGRGVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALI 86  
DB 15 LCVAWASSDRQCHQSPPLISG--TWKVSTGGHDLASGEFSYDSKANKRFVEDAAHAN 72

QY 87 PKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQPMWDLDPONSTFEDQYSIGGP---Q 143  
DB 73 KTSHT-DVLVHPEEGTLYEIDSKNESCKKLTQFRKHLMEIPDPATHESEIYWGSPSITE 131

QY 144 EQITVQWSDRKARSYETWIGYTVKDCYVPQETFTINYSVILSTRFPDIQIGIKDPSV 203  
DB 132 QGLURVRWVGKLPHELHAHYSLSI-TSCGCLPVSGSYGDKKOLLFS-FFGVETEVDLQV 189

QY 204 FTPPSTCOMAQLKMSGDCSW 224  
DB 190 FVPPAYCEGVAFPEAPDDHSF 210

RESULT 9  
E70834  
probable regulatory protein with some - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: E70834  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: E70834  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1085 <COL>  
A;Cross-references: UNIPROT:O53720; UNIPARC:UPI000016521A; GB:AL021931; GB:AL123456; NID  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: RV0386

Query Match 7.2%; Score 87; DB 2; Length 1085;  
Best Local Similarity 23.3%; Pred. No. 6.5;  
Matches 67; Conservative 36; Mismatches 88; Indels 96; Gaps 16;

QY 2 PGRAPLRTVPGLGAW-----LLGGLMAWTLCGLCS-----LGAVGA 38  
DB 256 PDLVPV-TVAGALGHDQGRSTDTVFLFGLGRPALVLDNCEHLLDATALVLA VKA 314

QY 39 PR-----PCQAPQWEGRGVMYQ-QSSGRNSRALLSYDGLNQRV----RVLDERKALIP 87  
DB 315 CRGVRLATCREPLRVEG-EVSVRVPSLSLSDAEMFCYRAQVRPDRFLTDNNSAAVT 373

QY 88 --CKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQPMWDLDPONSTFEDQYSI--GGPQ 143  
DB 374 EICKRL-----DGLPLAIELAAARLSMTLDEIIDGL-----RDRFALLTGGAR 417

QY 144 EQITVQ-----EWS-----DRKSARSYETWIGYTVKDCYVPV-----Q 176  
DB 418 TAAHQOTLWASVDWSTLTTEPERILFRFLAVFGCFVDDQAQVACSGDVQRYQVLDE 477

QY 177 EFTFTINYSVILSTRFPDIQIGIKDPSVFTPPSTCOMAQMAQ---LEKMS 220  
DB 478 IITLVKSLVMA-----DDNSGRTCYRLCETMRHYALEKLS 514

RESULT 10  
S75644  
hypothetical protein sll1885 - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S75644  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S75644  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-845 <KAN>  
A;Cross-references: UNIPROT:P74119; UNIPARC:UPI00000C1006; EMBL:D90912; GB:AB001339; NID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Genetics:  
A;Start codon: GTG  
C;Superfamily: Synechocystis hypothetical protein sll1885

Query Match 6.9%; Score 84; DB 2; Length 845;  
Best Local Similarity 19.5%; Pred. No. 9.3;  
Matches 56; Conservative 42; Mismatches 103; Indels 86; Gaps 11;

QY 12 GALGAWLLGGLWAWTL--CGLCSLGAVGAP-----RPC----- 42  
DB 16 GLLGAWLVLGANSSNTDHHGISSPSALADPPPNQKISPVTQNDYSSIFSPATLVS 75

QY 43 QAPQWEGRGVMYQSS-----SGRNSRALLSYDGLNQRVRLD 80  
DB 76 QRPSSGRSGRSILMVEAEEDNFAVLQAVTLTVDNVILHNGQQTAABELTLDSTRNRLALVV 135

QY 81 ERKAL--IPCKR-----LFEYLLYKDGVMFQIDQATKQCSKMTLTQPMW----- 123  
DB 136 EGVKLADSPINQDNAGPDTLMKRLRIK-----QLDRGVVEVSLNAQEQSVTVRSHNQ 190

QY 124 -----PLDIPONS---TFEDQYSIG--GPQEQITVQWSDRKARSYETWIGYTVKDCY 173  
DB 191 GILLAPTATAETAETLEIKDEVSQGELSPEETLILSQTDAIDGARVEETSVETTTTES-- 248

QY 174 PVQETFTINYSVILSTRFPDIQIGIKDPSVFTPPSTCOMAQLEKMS 220  
DB 249 -AONGITESSDLNQNTGLDIITGPTEPTISSEESTVNVLETQREND 294

RESULT 11  
S10326  
alpha-antigen A, extracellular - Mycobacterium bovis  
C;Species: Mycobacterium bovis  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S10326; B41499  
R;de Wit, L.; de la Cuvelier, A.; Ooms, J.; Content, J.  
Nucleic Acids Res. 18, 3995, 1990  
A;Title: Nucleotide sequence of the 32 kDa-protein gene (antigen 85 A) of Mycobacterium  
A;Reference number: S10326; MUID:90326531; PMID:2197602  
A;Accession: S10326  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-338 <WIT>  
A;Cross-references: UNIPROT:P17944; UNIPARC:UPI000002CE66; EMBL:X53034; NID:944165; PID  
R;Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M.  
Infect. Immun. 58, 272-274, 1990  
A;Title: Evidence for three separate genes encoding the proteins of the mycobacterial a  
A;Reference number: A41499; MUID:90093478; PMID:2403534  
A;Accession: B41499  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 44-82 <WIK>  
A;Cross-references: UNIPARC:UPI00000AP800  
C;Superfamily: Mycobacterium avium alpha-antigen

Query Match 6.8%; Score 83; DB 2; Length 338;  
Best Local Similarity 40.0%; Pred. No. 3.8;  
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;



C:Species: Homo sapiens (man)  
C:Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 09-Jul-2004  
C:Accession: E59435  
C:Accession: E59435  
R:Gorman, S.W.; Haider, N.B.; Grieshammer, U.; Swiderski, R.E.; Kim, E.; Welch, J.W.; Se-  
Genomics 59, 150-160, 1999  
A:Title: The cloning and developmental expression of unconventional myosin IXA (MYO9A) a  
A:Reference number: E59435  
A:Accession: E59435  
A:Status: preliminary  
A:Molecule type: DNA  
A:Molecule type: DNA  
A:Residues: 1-2548 <GOR>  
A:Cross-references: UNIPROT:O9UNJ2; UNIPARC:UPI0000007206F; GB:NP\_008832; PID:q55902012; E

Query Match	6.5%; Score 79.5; DB 2; Length 2548;
Best Local Similarity	20.2%; Pred. No. 96;
Matches 39; Conservative 26; Mismatches 77; Indels 51; Gaps 7;	
Qy	41 PCQAPQWQEGRVQMVQOSSGRNSRALI-----SYDGLNQVRVLDERKALIPCKRL 91
Db	82 PVQOMLWP-RMALENRLSGEDYFLREKNLDCGSIHYGSLQSLWLRVTEERRMM--ERG 138
Qy	92 FEYILLYKDGVMFOIDQATKCCXMTLTQPWDPLDIPQNSTFEQYSIGGQEQOITVOEW 151
Db	139 F-----LFQOQKQDFDCLCSLPDLNEXYTLLENL 166
Qy	152 SDRKSARSYETWIG-IYTVKDCYVQOETFTINYSVILSTRFFD-IQLGIDKDPSPVTPST 209
Db	167 RDRFHEKIYTVGSGILIVNPFKFLPIYNPKY-----VKMYDNHQKQKPEPHIYAVDV 221
Qy	210 CQMAQLEKMSEDC 222
Db	222 AYHAMLORKKNQC 234

Search completed: June 10, 2006, 02:57:39  
Job time : 46 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 10, 2006, 02:48:39 ; Search time 296 seconds  
(without alignments)  
700.012 Million cell updates/sec

Title: US-10-733-646-2  
Perfect score: 1214  
Sequence: 1 MFCRAPLRTVPCALGAWLLG.....TPPSTCQMAQLEKMSDSCSW 224

Scoring table: BLOSUM62

Gapop.10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1214	100.0	224	1	EPDR1_HUMAN
2	1206	99.3	344	1	Q96J80_homo sapien
3	1194	98.4	224	2	Q9M77_MOUSE
4	1168	96.2	227	2	Q95K54_MACFA
5	1164	95.9	224	1	EPDR1_MACFA
6	1164	95.9	227	2	Q95K77_MACFA
7	1102.5	90.8	218	2	Q95K56_MACFA
8	1000	82.4	224	2	Q9M71_MOUSE
9	994	81.9	224	2	O8CA12_MOUSE
10	993	81.8	224	2	O5X110_RAT
11	986	81.2	224	2	Q8BQ11_MOUSE
12	683.5	56.3	206	2	Q6DH25_BRARE
13	434.5	35.8	234	2	Q6E8F4_9ECHN
14	288	23.7	194	2	Q6IWN5_BRARE
15	192.5	15.9	221	1	EPD2_ONCMY
16	192	15.8	211	2	Q4TFW4_TETNG
17	190.5	15.7	221	1	EPD1_ONCMY
18	189.5	15.6	221	1	EPD2_SALSA
19	185.5	15.3	221	1	EPD_ESOLU
20	181	14.9	181	2	Q90394_9TELE
21	177	14.6	178	2	Q91083_9TELE
22	174.5	14.4	175	2	Q91140_9TELE
23	173	14.3	178	2	Q91253_9TELE
24	173	14.3	181	2	Q91109_9TELE
25	172	14.2	178	2	Q91052_9TELE
26	167.5	13.8	215	1	EPD_CYBCA
27	164.5	13.6	183	2	Q90492_9TELE
28	163.5	13.5	212	1	EPD_CLUHA
29	159	13.1	218	1	EPD_DANAE
30	158	13.0	214	1	EPD_NOTCH
31	157.5	13.0	216	2	Q4S8U8_TETNG

32 156.5 12.9 215 1 EPD1\_CARAU  
33 154.5 12.7 217 1 EPD\_BRARE  
34 154 12.7 180 2 Q91331\_9TELE  
35 153.5 12.6 215 1 EPD2\_CARAU  
36 152.5 12.6 186 2 Q91465\_9TELE  
37 148 12.2 170 2 Q90241\_9TELE  
38 147.5 12.1 136 2 Q91254\_9TELE  
39 146 12.0 172 2 Q91057\_9TELE  
40 132.5 10.9 140 2 Q91045\_9TELE  
41 131 10.8 203 2 Q6WNG6\_BRARE  
42 129.5 10.7 131 2 Q90276\_9TELE  
43 125.5 10.3 137 2 Q91056\_9TELE  
44 125 10.3 192 2 Q91464\_9TELE  
45 123 10.1 133 2 Q91059\_9TELE

#### ALIGNMENTS

#### RESULT 1

EPDR1\_HUMAN STANDARD; PRT; 224 AA.  
AC Q9UM22;  
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.  
DT 21-FEB-2006, sequence version 2.  
DT 07-FEB-2006, entry version 40.  
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1  
DE protein).  
DE Names=EPDR1; Synonyms=MERP1, UCC1;  
GN Homo sapiens (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,  
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;  
RT "Identification and characterization of a novel family of mammalian  
RT endymmin-related proteins (MERPs) in hematopoietic, nonhematopoietic,  
RT and malignant tissues.";  
RL DNA Cell Biol. 20:625-635(2001).  
[2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Cervix;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 51-224.  
RA Niamrich I., Erdmann S., Melchers U.;  
RT "Genes that are differentially expressed in colon cancer.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Secreted protein.

CC -1- SIMILARITY: Belongs to the ependymin family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL: AF361252; AAK26441.1; -; Genomic DNA.  
CC ENBL: BC000686; AAH00686.2; ALT\_INIT; mRNA.  
CC ENBL: BC018299; AAH18299.1; -; mRNA.  
CC ENBL: AJ250475; CAB60269.1; ALT\_INIT; mRNA.  
CC DR Ensembl: ENSG00000086289; Homo sapiens.  
CC DR HGNC: HGNC:17572; EPDR1.  
CC DR LinkHub: Q9UM22; -.  
CC DR InterPro: IPR001299; Ependymin.  
CC DR PANTHER: PTHR10697; Ependymin; 1.  
CC DR PRINTS: PR00317; EPENDYMIN.  
CC DR ProDom: PD006315; Ependymin; 1.  
CC DR PROSITE: PS00898; EPENDYMIN\_1; 1.  
CC DR PROSITE: PS00899; EPENDYMIN\_2; 1.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 37 Potential.  
FT CHAIN 38 224 Mammalian ependymin-related protein 1.  
FT /FTId=PRO\_0000008351.  
FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 207 207 P -> S (in Ref. 3).  
SQ SEQUENCE 224 AA; 25437 MW; 84ADBA366261611 CRC64;  
  
Query Match 100.0%; Score 1214; DB 1; Length 224;  
Best Local Similarity 100.0%; Pred. No. 9.3e-107;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MFGAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRGVYQSSG 60  
DB 1 MFGAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRGVYQSSG 60  
  
QY 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120  
DB 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120  
  
QY 121 PWDPLDIPNSTFEDQYSIGGPQEQITVQWSDRSARSYETWIGIYTKDCYPVQETFT 180  
DB 121 PWDPLDIPNSTFEDQYSIGGPQEQITVQWSDRSARSYETWIGIYTKDCYPVQETFT 180  
  
QY 181 INYSVILSTRFFDIQIGKIDPSVFTPTSTCQMAQLEKMSDCSW 224  
DB 181 INYSVILSTRFFDIQIGKIDPSVFTPTSTCQMAQLEKMSDCSW 224  
  
RESULT 2  
Q96J80 HUMAN PRELIMINARY; PRT; 344 AA.  
AC Q96J80;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE Mammalian ependymin related protein 1.  
GN Name=EPDR1; Synonyms=MERP1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,  
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;  
RT "Identification and characterization of a novel family of mammalian  
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,  
RT and malignant tissues."  
RL DNA Cell Biol. 20:625-635(2001).  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=21940632; PubMed=11943480; DOI=10.1016/S0378-1119(02)00434-1;  
RA Gregorio-King C.C., McLeod J.L., Collier F.M., Collier G.R.,  
RA Bolton K.A., Van Der Meer G.J., Apostolopoulos J., Kirkland M.A.;  
RT "MERP1: a mammalian ependymin-related protein gene differentially  
RT expressed in hematopoietic cells."  
RL Gene 286:249-257(2002).  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL: AY027862; AAK15788.2; -; mRNA.  
CC DR Ensembl: ENSG00000086289; Homo sapiens.  
CC DR HGNC: HGNC:17572; EPDR1.  
CC DR LinkHub: Q96J80; -.  
CC DR GO: GO:0005576; C:extracellular region; IEA.  
CC DR GO: GO:0005509; F:calcium ion binding; IEA.  
CC DR GO: GO:0007160; P:cell-matrix adhesion; IEA.  
CC DR InterPro: IPR001299; Ependymin.  
CC DR PANTHER: PTHR10697; Ependymin; 1.  
CC DR PRINTS: PR00317; EPENDYMIN.  
CC DR ProDom: PD006315; Ependymin; 1.  
CC DR PROSITE: PS00898; EPENDYMIN\_1; UNKNOWN 1.  
SQ SEQUENCE 344 AA; 38141 MW; 34D75B84822692DA CRC64;  
  
Query Match 99.3%; Score 1206; DB 2; Length 344;  
Best Local Similarity 99.6%; Pred. No. 8.8e-106;  
Matches 223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MFGAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRGVYQSSG 60  
DB 121 MFGAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRGVYQSSG 180  
  
QY 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120  
DB 181 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 240  
  
QY 121 PWDPLDIPNSTFEDQYSIGGPQEQITVQWSDRSARSYETWIGIYTKDCYPVQETFT 180  
DB 241 PWDPLDIPNSTFEDQYSIGGPQEQITVQWSDRSARSYETWIGIYTKDCYPVQETFT 300  
  
QY 181 INYSVILSTRFFDIQIGKIDPSVFTPTSTCQMAQLEKMSDCSW 224  
DB 301 INYSVILSTRFFDIQIGKIDPSVFTPTSTCQMAQLEKMSDCSW 344  
  
RESULT 3  
Q99M77 MOUSE PRELIMINARY; PRT; 224 AA.  
AC Q99M77;  
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2001, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE Mammalian ependymin related protein 1.  
GN Name=Ucc1; Synonyms=Epdr1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Thymus;  
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,  
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;  
RT "Identification and characterization of a novel family of mammalian  
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,  
RT and malignant tissues."  
RL DNA Cell Biol. 20:625-635(2001).  
CC -----  
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```
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CC -----
DR EMBL; AY027861; AAK15787.1; -; mRNA.
DR MGI; MGI-2152290; Epdrl.
DR MGI; MGI-2152290; Ucc1.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD066315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
SQ SEQUENCE 224 AA; 25437 MW; DB6A5A9A7289E95 CRC64;

Query Match 98.4%; Score 1194; DB 2; Length 224;
Best Local Similarity 99.1%; Pred. No. 7.3e-105;
Matches 222; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRCPQAPQWQEGRVQVYQSSG 60
DB 1 MPRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRCPQAPQWQEGRVQVYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQVSGIGPQEQITVQWSDRSKARSYETWIGYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQVSGIGPQEQITVQWSDRSKARSYETWIGYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQIGIKDPSVFTPTSTCMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQIGIKDPSVFTPTSTCMAQLEKMSDCSW 224

RESULT 4
Q95K54 MACFA PRELIMINARY; PRT; 227 AA.
AC Q95K54;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the ependymin family.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AB066537; BAB62213.1; -; mRNA.
CC GO; GO:0005576; C:extracellular region; IEA.
CC GO; GO:0005509; F:calcium ion binding; IEA.
CC GO; GO:0007160; P:cell-matrix adhesion; IEA.
CC InterPro; IPR001299; Ependymin.
CC PANTHER; PTHR10697; Ependymin; 1.
CC PRINTS; PR00317; EPENDYMIN.
CC ProDom; PD066315; Ependymin; 1.
CC PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
CC PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.
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SQ SEQUENCE 227 AA; 25850 MW; 3963EAB6D5F016F4 CRC64;

Query Match 96.2%; Score 1168; DB 2; Length 227;
Best Local Similarity 96.0%; Pred. No. 2.2e-102;
Matches 215; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRCPQAPQWQEGRVQVYQSSG 60
DB 4 MPRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRCPQAPQWQEGRVQVYQSSG 63
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 64 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 123
QY 121 PWDPLDIPQNSTFEDQVSGIGPQEQITVQWSDRSKARSYETWIGYTVKDCYPVQETFT 180
DB 124 PWDPLDIPQNSTFEDQVSGIGPQEQITVQWSDRSKARSYETWIGYTVKDCYPVQETFT 183
QY 181 INYSVILSTRFFDIQIGIKDPSVFTPTSTCMAQLEKMSDCSW 224
DB 184 KNYSVILSTRFFDIQIGIKDPSVFTPTSTCMAQLEKMSDCSW 227

RESULT 5
EPDR1 MACFA STANDARD; PRT; 224 AA.
ID EPDR1 MACFA
AC Q9NOC7;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 21-FEB-2001, sequence version 2.
DT 07-FEB-2006, entry version 31.
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1
DE protein).
GN Names=EPDR1; Synonyms=MERP1, UCC1; ORFNames=QcE-12983;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the ependymin family.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AB046003; BAB01585.1; ALT_INIT; mRNA.
CC LinkHub; Q9NOC7;
CC InterPro; IPR001299; Ependymin.
CC PANTHER; PTHR10697; Ependymin; 1.
CC PRINTS; PR00317; EPENDYMIN.
CC ProDom; PD066315; Ependymin; 1.
CC PROSITE; PS00898; EPENDYMIN_1; 1.
CC PROSITE; PS00899; EPENDYMIN_2; 1.
CC Glycoprotein; Signal.
FT SIGNAL 1 37 Potential
FT CHAIN 38 224 Mammalian ependymin-related protein 1.
FT /FTID=PRO_000008352.
FT CARBOHYD 130 130 N-linked (GLNAC...) (Potential).
FT CARBOHYD 182 182 N-linked (GLNAC...) (Potential).
SQ SEQUENCE 224 AA; 25484 MW; 3594311D15AB4BB7 CRC64;

Query Match 95.9%; Score 1164; DB 1; Length 224;
Best Local Similarity 96.0%; Pred. No. 5.2e-102;
Matches 215; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MPRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVGAPRCPQAPQWQEGRVQVYQSSG 60
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Db 1 MFGRAPLRTVPGALGAWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 60
61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKQCSKMTLT 120
121 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRSKARSYETWIGIYTVKDCYPVOETFT 180
121 PWDPLDIPONSTFEDQYSIGGPOEQIMVQWSDRSKARSYETWIGIYTVKDCYPVOETFT 180
181 INYSVILSTRFRFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224
181 KNYSVILSTRFRFDIQLGKIDPSVFTPPSTCQIAQLEKMSDCSW 224
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## RESULT 6

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Q95K77 MACFA
ID Q95K77 MACFA PRELIMINARY; PRT; 227 AA.
AC Q95K77;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Temporal lobe right;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
RA Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RT chromosomes.";
RL Gene 275:31-37(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
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EMBL; AB063094; BAB60800.1; -; mRNA.
DR EMBL; AB097520; BAC41745.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25821 MW; BE6A77C5867DA50A CRC64;

Query Match 95.9%; Score 1164; DB 2; Length 227;
Best Local Similarity 96.0%; Pred. No. 5.3e-102;
Matches 215; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
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QY 1 MFGRAPLRTVPGALGAWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 60
Db 4 MFGRAPLRTVPGALGAWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 63
61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
64 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKQCSKMTLT 123
121 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRSKARSYETWIGIYTVKDCYPVOETFT 180
124 PWDPLDIPONSTFEDQYSIGGPOEQIMVQWSDRSKARSYETWIGIYTVKDCYPVOETFT 183
181 INYSVILSTRFRFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224
184 KNYSVILSTRFRFDIQLGKIDPSVFTPPSTCQIAQLEKMSDCSW 227
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## RESULT 7

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Q95K56 MACFA
ID Q95K56 MACFA PRELIMINARY; PRT; 218 AA.
AC Q95K56;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AB066535; BAB62211.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 218 AA; 24970 MW; 8B8524C0D986677C CRC64;
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Query Match 90.8%; Score 1102.5; DB 2; Length 218;
Best Local Similarity 92.0%; Pred. No. 3.5e-96;
Matches 206; Conservative 4; Mismatches 5; Indels 9; Gaps 1;

QY 1 MFGRAPLRTVPGALGAWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 60
Db 4 MFGRAPLRTVPGALGAWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 54
61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
55 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKQCSKMTLT 114
121 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRSKARSYETWIGIYTVKDCYPVOETFT 180
115 PWDPLDIPONSTFEDQYSIGGPOEQIMVQWSDRSKARSYETWIGIYTVKDCYPVOETFT 174
181 INYSVILSTRFRFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224
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Db 175 KNSVILSTRFFDTQLGKIDPSVFTPBTPCQIAQLEKMSDCSW 218

# RESULT 8

ID Q99M71\_MOUSE PRELIMINARY; PRT; 224 AA.  
AC Q99M71;  
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 29.  
DE Mammalian ependymin related protein-2 (Ependymin 2) (Adult male  
DE diencephalon cDNA, RIKEN full-length enriched library,  
DE clone:9330154O03 product:mammalian ependymin related protein-2) (Adult  
DE male cerebellum cDNA, RIKEN full-length enriched library,  
DE clone:1500034M21 product:Mammalian ependymin related protein-2  
DE (Similar to mammalian ependymin related protein 1), full insert  
DE sequence).  
GN Name:Epdr2; Synonyms:A0040950, MERP2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J and C57BL/6J;  
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,  
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;  
RT "Identification and characterization of a novel family of mammalian  
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,  
RT and malignant tissues";  
RL DNA Cell Biol. 20:625-635 (2001).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=FVB/N; TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares T.B., Tonhuyuk S., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,  
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=FVB/N; TISSUE=Kidney;  
RC Director MGC Project;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning";  
RL Methods Enzymol. 303:19-44 (1999).  
RN [5]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells S., Kodzius R., Shimokawa K.,  
RA Davis V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
RA Fletcher C.P., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,  
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris L.,  
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Seesla L.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Tesardale R.D., Liu E.T., Bruscia V., Quackenbush J.,  
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Tida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimmiya N.,  
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome";  
RL Science 309:1559-1563 (2005).  
RN [6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RC RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome";  
RL Science 309:1564-1566 (2005).  
RN [7]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nigado I., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,  
RA Balla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Wiki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Yanagisawa M., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Iehii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sesaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston K., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=21085660; PubMed=111217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Iehii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT Prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
RA Sumi N., Iehii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Query Match 82.4%; Score 1000; DB 2; Length 224;  
Best Local Similarity 80.3%; Pred. No. 1.9e-86;  
Matches 179; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
QY 1 MFCRAPLRTPVPGALGAWLLGGLMAWTLGCLSLGAVGAPRCPQAPQOWEGRWVYQSSG 60  
DB 1 MPBARPRRLVQVGRGTWLLGSLVWVWVLLGSLMAGSLGTTPQCPQAPQOWEGRWVYQSSG 60  
QY 61 RNSRALLSVGLNQRVRVLDERKALIPCKRLFEYILLYKGVWFQIDQATKCSKWTLTQ 120  
DB 61 HNNRALVSVGLNQRVRVLDERKALIPCKRLFEYILLYKGVWFQIDQATKCAKIPLVE 120  
QY 121 PWDPLDIPQNSTFEDQYSIGGGQEQILVQEWSDRRTSARSETWIGTYTAKDCVPVQETFT 180

DB 121 SWDPLDIPQNSTFEDQYSIGGGQEQILVQEWSDRRTSARSETWIGTYTAKDCVPVQETFT 180  
QY 181 INYSVILSTRFRFDIOLIGIKNDPSVFTPTSTCQMAQLEKMSDECS 223  
DB 181 RNYTVVMSTRFRFDVQLGINKDPSVFTPTSTCQAAQPEKMSDGS 223  
RESULT 9  
Q8CA12 MOUSE PRELIMINARY; PRT; 224 AA.  
ID Q8CA12;  
AC 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DE Adult male hypothalamus cDNA, RIKEN full-length enriched library,  
DE clone: A230058H08 product: MAMMALIAN EPENDYMIN RELATED PROTEIN-2  
DE (SIMILAR TO MAMMALIAN EPENDYMIN RELATED PROTEIN 1) homolog.  
GN Name=EpdR2; Synonym=AU040950;  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44 (1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Implombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA Fleischer C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H.,  
RA Kitano H., Kollias G., Kriehnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurchkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Mattagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugimura K., Sultana R., Takenaka Y., Taki K.,  
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamashiki H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brueic V., Quackenbush J.,  
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kohjima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami T., Waki K., Watanishi A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";

```

Science 309:1559-1563(2005).
[3]
RT NUCLEOTIDE SEQUENCE.
RN
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC PubMed=16141073; DOI=10.1126/science.1112009;
RX RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RN Science 309:1564-1566(2005).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guetinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou R.D., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R.G., Wagner L., Watanabe C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.
RT "Analysis of the mouse transcriptome based on functional annotation of
RN 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Browne M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtauki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.
RT "Normalization and subtraction of cap-trapper-selected cDNAs to

```

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RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RN sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takeda F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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-----
CC EMBL; AK038733; BAC30113.1; -; mRNA.
DR Ensembl; ENSMUSG00000002808; Mus musculus.
DR MGI; MGI:2145369; AU040950.
DR MGI; MGI:2145369; Eppd2.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0005509; F:calcium ion binding; RCA.
DR GO; GO:0007160; P:cell-matrix adhesion; RCA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00000; Ependymin; 1.
SQ SEQUENCE 224 AA; 25515 MW; D49BAC6C8A4857BB CRC64;

Query Match 81.9%; Score 994; DB 2; Length 224;
Best Local Similarity 79.8%; Pred. No. 7.2e-86;
Matches 178; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

QY 1 MFCRAPLRTVPGALGAWLLGGLNWLTCGLCSLGAVCAPRCPQAPQWEGRWVYQSSG 60
DB 1 MPAPAPRLVQGRGTWLLGSLVWVWVLCGLMGAGSLGTGPQAPQWEGRWVYQSSG 60
QY 61 RNSRALSYDGLNQRVRVLDERKALIPCKRLFFVILLYKGVWFQIDQATKQCSKMTLQ 120
DB 61 HNNRALVSDGLNQRVRVLDERKALIPCKRLFFVILLYKGVWFQIDQATKQCAKIPVE 120
QY 121 PWDPLDIPQNSTFEDQYSGGPOEQITVQWSDRKSARSYETWIGIVTKDCYPVQETFT 180
DB 121 SWDPLDIPQNSTFEDQYSGGPOEQITVQWSDRKSARSYETWIGIVTKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGIKDPSPVFTPTSTCOMAQLEKMSDCS 223
DB 181 RNYTVVMSTRFFDVLQSLIKDPSPVFTPTSTCOMAQLEKMSDCS 223

RESULT 10
Q5X110_RAT
ID Q5X110_RAT PRELIMINARY; PRT; 224 AA.
AC Q5X110;

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RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schraml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Ponting J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Watanabe R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaado I., Pesole G., Quackenbush J.,  
 RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).

RN [7]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matakiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RN Genome Res. 10:1757-1771(2000).

RN [8]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akai H., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL; AK046185; BAC32624.1; -; mRNA.

DR Ensembl; ENSMUSG00000002808; Mus musculus.

DR MGI; MGI:2145369; AU040950.

DR MGI; MGI:2145369; Epub2.

DR GO; GO:0005615; C:extracellular space; RCA.

DR GO; GO:0005509; F:calcium ion binding; RCA.

DR GO; GO:0007160; P:cell-matrix adhesion; RCA.

DR InterPro; IPR001299; Ependymin.

DR PANTHER; PTHR10697; Ependymin; 1.

DR PRINTS; PR00317; Ependymin.

DR ProDom; PD006315; Ependymin; 1.

SQ SEQUENCE 224 AA; 25386 MW; 65DEB828B485111 CRC64;

Query Match 81.2%; Score 986; DB 2; Length 224;

Best Local Similarity 79.8%; Pred. No. 4.2e-85;

Matches 178; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MPRAPRLTPVPGALGAWLLGGLWAWTLCGLSGVAGCAPRCPQAPQWEGRQVLYQSSG 60

Db 1 MPRAPRLTPVPGALGAWLLGGLWAWTLCGLSGVAGCAPRCPQAPQWEGRQVLYQSSG 60

Qy 61 RNSRALLSYDGLNORVRVLDERKALIPCKELFEVILLYKGVFQIDQATKQCKSWTLTQ 120

Db 61 HNNRALVSVDGLNORVRVLDERKALIPCKELFEVILLYKGVFQIDQATKQCKSWTLTQ 120

Qy 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180

Db 121 SSDPLDIPQNSTFEDQYSIGGPOEQILVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180

Qy 181 INYSVILSTRFFDIQGIKDPSPVTPPSTCMAQLEKMSDSCS 223

Db 181 RNYTVVMSTRFFDVQLGIKDPSPVTPPSTCMAQLEKMSDSCS 223

RESULT 12

Q6DH25\_BRARE

ID Q6DH25\_BRARE PRELIMINARY; PRT; 206 AA.

AC Q6DH25;

DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.

DT 16-AUG-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Ependymin related protein 1.

GN Name=epdrl;

OS Brachydanio rerio (Zebrafish) (Danio rerio).





FT	CARBOHYD	33	33	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	73	73	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	97	97	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	221 AA;	24467 MW; 7931COBCAD24ABB3 CRC64;	
	Query Match	15 9#;	Score 192.5; DB 1; Length 221;	
	Best Local Similarity	25.0#;	Pred No. 9.2e-10;	
	Matches	49; Conservative	39; Mismatches 103; Indels	5; Gaps
Qy	25	WTLGLCLSLGAVGRPCQPQQWEGRQVMYQQSSGRNSRALLSYDGUNQRVRLDERKA	84	
Db	12	WLCLGATAEAESHGPOHCTSNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRFTESEMH	71	
Qy	85	LIPCKRLFAYILLKYKGVMFQIDQATKCCKSWTILTPQWDPLDIQNPSFEDQYSTGG---	141	
Db	72	LNKTEHLUDYLMLPEEFGVFYDIDMKNSCKKNLSHSHAHLELPAGAQAHVFLGSDTV	131	
Qy	142	PQEQTIVQENSDRKSARSYETWIGIYTKDCYPVQETETINYSVILSTRFFFIQLGIKD	201	
Db	132	QEDNIKVINWG-SVAETKGQYSALTTVGECLPL-STFYSTDITLLFSNSEVVTEVKAP	189	
Qy	202	SVFTPPTCQMAOLEK	217	
Db	190	EMFTLPSCFAVELEE	205	

Search completed: June 10, 2006, 02:56:51  
Job time : 299 secs

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; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Human
US-09-242-890-11

Query Match      100.0%; Score 1214; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-132;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPPCQAPQWEGRQVMYQSSG 60
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPPCQAPQWEGRQVMYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
Db 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180
Db 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLEKMSDCSW 224
Db 181 INYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLEKMSDCSW 224
```

```
RESULT 3
US-10-187-904-2
; Sequence 2, Application US/10187904
; Patent No. 6683161
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCES: Pf403D1
; CURRENT APPLICATION NUMBER: US/10/187,904
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-187-904-2

Query Match      100.0%; Score 1214; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-132;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPPCQAPQWEGRQVMYQSSG 60
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPPCQAPQWEGRQVMYQSSG 60
```

```
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
Db 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180
Db 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLEKMSDCSW 224
Db 181 INYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLEKMSDCSW 224
```

```
RESULT 4
US-09-242-890-10
; Sequence 10, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Human
US-09-242-890-10
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Query Match      89.0%; Score 1081; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGCLSLGAVGAPPCQAPQWEGRQVMYQSSGRNRRALLSYDGLNQRVRLDERKA 84
Db 1 WTLGCLSLGAVGAPPCQAPQWEGRQVMYQSSGRNRRALLSYDGLNQRVRLDERKA 60
QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQE 144
Db 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQE 120
QY 145 QITVQWSDRKSARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVF 204
Db 121 QITVQWSDRKSARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVF 180
QY 205 TTPSTCQMAQLEKMSDCSW 224
Db 181 TTPSTCQMAQLEKMSDCSW 200
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```
RESULT 5
US-09-242-890-1
; Sequence 1, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
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; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 1  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Human  
US-09-242-890-1

Query Match 82.8%; Score 1005; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.8e-108;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 APPRCPAQQWEGQVQVQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILL 97  
DB 1 APPRCPAQQWEGQVQVQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILL 60  
QY 98 YKDGVMFQIDQATKQCSKMTLTQPDLDIPONSTFEDQYSIGGPOEQITVQWSDRKS 157  
DB 61 YKDGVMFQIDQATKQCSKMTLTQPDLDIPONSTFEDQYSIGGPOEQITVQWSDRKS 120  
QY 158 RSYETWIGIVTKDCYVQVQFTTINYSVILSTRFFDIQIGKDPSPVTPPSTCMAQLEK 217  
DB 121 RSYETWIGIVTKDCYVQVQFTTINYSVILSTRFFDIQIGKDPSPVTPPSTCMAQLEK 180  
QY 218 MSEDSCW 224  
DB 181 MSEDSCW 187

RESULT 6  
US-09-242-890-13  
; Sequence 13, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 13  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-242-890-13

Query Match 82.4%; Score 1000; DB 2; Length 224;  
Best Local Similarity 80.3%; Pred. No. 8.9e-108;  
Matches 179; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
QY 1 MPCRPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRCPAQQWEGQVQVQSSG 60  
DB 1 MPAPARRLVQGRGTWLLGSLVWVLCGLMGAGSLGTPOPCAPQWEGQVLYQSSG 60  
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120

DB 61 HNNRALVSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCAKIPLVE 120  
QY 121 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGIVTKDCYVQVQFTT 180  
DB 121 SWDPLDIPONSTFEDQYSIGGPOEQILVQWSDRRRTARSYETWIGIVTKDCYVQVQFTFI 180  
QY 181 INYSVILSTRFFDIQIGKDPSPVTPPSTCMAQLEKMSDSCS 223  
DB 181 RNYTVVMSTRFFDVQLGKIDPSPVTPPSTCQAAQPEKMSDSCS 223

RESULT 7  
US-09-242-890-12  
; Sequence 12, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 12  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-242-890-12

Query Match 81.8%; Score 993; DB 2; Length 224;  
Best Local Similarity 81.8%; Pred. No. 5.8e-107;  
Matches 180; Conservative 15; Mismatches 25; Indels 0; Gaps 0;  
QY 4 RAPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRCPAQQWEGQVQVQSSGRNS 63  
DB 4 RAPRLVQGPRETWLLGGLWVWLICGLMGAGSPGTPOPCAPQWEGQVLYQSSGHS 63  
QY 64 RALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQPWD 123  
DB 64 RALVSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCAKIPLAEFPD 123  
QY 124 PLDIPONSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGIVTKDCYVQVQFTTINY 183  
DB 124 PLDIPONSTFEDQYSIGGPOEQIMVQWSDRRRTARSYETWIGIVTKDCYVQVQFTIRNY 183  
QY 184 SVILSTRFFDIQIGKDPSPVTPPSTCMAQLEKMSDSCS 223  
DB 184 TVVLSTRFFDVQLGKIDPSPVTPPSTCQTAQPEKMKENS 223

RESULT 8  
US-09-242-890-2  
; Sequence 2, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10

```
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-2

Query Match
Best Local Similarity 73.5%; Score 892; DB 2; Length 190;
Matches 161; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 37 GAPPQAPQWEGROWVQOSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYIL 96
DB 3 GTPQCAPQWEGROWVQOSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYIL 62
QY 97 LYKGVWFQIDQATKQCSKMTLTPWDPDIPONSTFEDQYSIGGPOEQLTVQWSDRKS 156
DB 63 LYKGVWFQIEQATKCAKIPLEPWPDPDIPONSTFEDQYSIGGPOEQLVWQENSDRRT 122
QY 157 ARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLE 216
DB 123 ARSYETWIGYTVKDCYPVQETFTIRNVTVMSTRFFDVQLGIKDPSPVFTPPSTCQTAQPE 182
QY 217 KMSDCS 223
DB 183 KMKENS 189
```

```
RESULT 9
US-09-242-890-3
; Sequence 3, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-3

Query Match
Best Local Similarity 72.1%; Score 875; DB 2; Length 187;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 39 PRPCQAPQWEGROWVQOSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYIL 98
DB 2 PQCQAPQWEGROWVQOSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYIL 61
QY 99 KGVWFQIDQATKQCSKMTLTPWDPDIPONSTFEDQYSIGGPOEQLTVQWSDRKSAR 158
DB 62 KGVWFQIEQATKCAKIPLVESWDPDIPONSTFEDQYSIGGPOEQLVQWSDRRTAR 121
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QY 159 SYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKM 218
DB 122 SYETWIGYTVKDCYPVQETFTIRNVTVMSTRFFDVQLGIKDPSPVFTPPSTCQAAQPEKM 181
QY 219 SEDCS 223
DB 182 SDGCS 186

RESULT 10
US-09-242-890-14
; Sequence 14, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-14
```

```
Query Match
Best Local Similarity 17.2%; Score 209; DB 2; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGAPLRTVPGALGAWLLGGLWAWTLGCLCSLGAVG 37
DB 1 MFGAPLRTVPGALGAWLLGGLWAWTLGCLCSLGAVG 37

RESULT 11
US-09-242-890-8
; Sequence 8, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like
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US-09-242-890-8

Query Match 16.6%; Score 201; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 5.4e-16;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 SYDGLNQRVRLDERKALIPCKRLFEYLLYKDGWMFQI 106  
Db 1 SYDGLNQRVRLDERKALIPCKRLFEYLLYKDGWMFQI 39

RESULT 12

US-09-229-583A-4  
; Sequence 4, Application US/09229583A  
; Patent No. 6489138  
; ORGANISM: Oncorhynchus mykiss  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin  
; FILE REFERENCE: PF403  
; CURRENT APPLICATION NUMBER: US/09/229,583A  
; CURRENT FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,330  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: US 60/075,278  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Oncorhynchus mykiss  
US-09-229-583A-4

Query Match 15.9%; Score 192.5; DB 2; Length 221;  
Best Local Similarity 25.0%; Pred. No. 7.8e-14;  
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

Qy 25 WTLGCLSLGAVGAPRCQAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKA 84  
Db 12 WLCGATALAESHGPOHCTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRTSEMH 71  
Qy 85 LIPCKRLFEYLLYKDGWMFQIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQYSIGG--- 141  
Db 72 LNKTEHLEDYLMLEFEGVFYDIDMKQSCCKMSLHSHAHLELPAGAHHQVELFLGSDTV 131  
Qy 142 PQEITVQWSDRSARSYETWIGIYTVKDCYPQVETFTINYSVILSTRFPDIOLGKDP 201  
Db 132 QEDNIKVINWVG-SVAETKQYSALTTVGECPL-STFYSTDSTITLLFSNSSEVVTEVKAP 189

Qy 202 SVETPSTCMAQLEK 217  
Db 190 EMFTLPSFCEAVELEE 205

RESULT 13

US-10-187-904-4  
; Sequence 4, Application US/10187904  
; Patent No. 6683161  
; ORGANISM: Human Ependymin  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin  
; FILE REFERENCE: PF403D1  
; CURRENT APPLICATION NUMBER: US/10/187,904  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 09/229,583  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,330  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: US 60/075,278  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4

; LENGTH: 221

; TYPE: PRT  
; ORGANISM: Oncorhynchus mykiss  
US-10-187-904-4

Query Match 15.9%; Score 192.5; DB 2; Length 221;  
Best Local Similarity 25.0%; Pred. No. 7.8e-14;  
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

Qy 25 WTLGCLSLGAVGAPRCQAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKA 84  
Db 12 WLCGATALAESHGPOHCTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRTSEMH 71  
Qy 85 LIPCKRLFEYLLYKDGWMFQIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQYSIGG--- 141  
Db 72 LNKTEHLEDYLMLEFEGVFYDIDMKQSCCKMSLHSHAHLELPAGAHHQVELFLGSDTV 131  
Qy 142 PQEITVQWSDRSARSYETWIGIYTVKDCYPQVETFTINYSVILSTRFPDIOLGKDP 201  
Db 132 QEDNIKVINWVG-SVAETKQYSALTTVGECPL-STFYSTDSTITLLFSNSSEVVTEVKAP 189  
Qy 202 SVETPSTCMAQLEK 217  
Db 190 EMFTLPSFCEAVELEE 205

RESULT 14

US-09-242-890-5  
; Sequence 5, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; APPLICANT: Onda, Haruo  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse ependym

Query Match 14.4%; Score 175; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.2e-13;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 QIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQ 136  
Db 1 QIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQ 32

RESULT 15

US-09-229-583A-5  
; Sequence 5, Application US/09229583A  
; Patent No. 6489138  
; ORGANISM: Human Ependymin  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin  
; FILE REFERENCE: PF403  
; CURRENT APPLICATION NUMBER: US/09/229,583A

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; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Cyprinus carpio
; US-09-229-583A-5

Query Match      13.8%; Score 167.5; DB 2; Length 215;
Best Local Similarity 24.4%; Pred. No. 6e-11;
Matches 50; Conservative 47; Mismatches 89; Indels 19; Gaps 8;

Qy   30 LCSLGAVGAPR-PCQAPQWEGRQVMYQSSGRNSRAL--LSYDGLNQVRVLDERKALI 86
Db   14 LCAVAWASSNRQCHSPPLTSG--TMKWSTGGHDLASGEFSYDSKANKRFVEDTAHAN 71
Qy   87 PCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPWDPLDIPONSTFDQYSIGGP---Q 143
Db   72 KTSHM-DVLVHPREGVLYEIDSKNESCKETLQFRKHLMEIPPDATHESEIYMGSPSITE 130
Qy   144 EQITVOEWSDR----XSARSYETWIGIYTVKDCYVPQOETFTINYSVILSTRFPDIOLGIK 199
Db   131 QGLRVRVWNGKLPCLHAHYSLST-----TSCGCLPVS GSYGDKDLIFS-FFGVETEVD 184
Qy   200 DPSVFTPPSTCQMAQLEKMSDCSW 224
Db   185 DPQVFVPPAYCEAVAFEEAPDDHSF 209
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Search completed: June 10, 2006, 02:58:31  
Job time : 51 secs

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: June 10, 2006, 02:57:54 ; Search time 185 seconds  
(without alignments)  
560.866 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 1214

Sequence: 1 MPCRPLRTVPGALGAWLLG.....TPPSTCQMAQLEKMSDCSW 224

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1214	100.0	224	4	US-10-612-788-11
2	1214	100.0	224	4	US-10-733-646-2
3	1214	100.0	224	5	US-10-733-646-2
4	1081	89.0	200	4	US-10-612-788-10
5	1005	82.8	187	4	US-10-612-788-11
6	1000	82.4	224	4	US-10-612-788-13
7	993	81.8	224	4	US-10-612-788-12
8	892	73.5	190	4	US-10-612-788-2
9	875	72.1	187	4	US-10-612-788-3
10	209	17.2	37	4	US-10-612-788-14
11	201	16.6	39	4	US-10-612-788-8
12	192.5	15.9	221	4	US-10-733-646-4
13	192.5	15.9	221	5	US-10-733-646-4
14	175	14.4	32	4	US-10-612-788-5
15	167.5	13.8	215	4	US-10-733-646-5
16	167.5	13.8	215	5	US-10-733-646-5
17	163.5	13.5	212	4	US-10-733-646-7
18	163.5	13.5	212	5	US-10-733-646-7
19	154.5	12.7	217	4	US-10-733-646-6
20	154.5	12.7	217	5	US-10-733-646-6
21	153.5	12.6	216	4	US-10-733-646-3
22	153.5	12.6	216	5	US-10-733-646-3
23	147	12.1	26	4	US-10-612-788-9
24	143	11.8	25	4	US-10-612-788-6
25	133	11.0	24	4	US-10-612-788-15
26	125	10.3	37	4	US-10-612-788-17
27	102	8.4	34	4	US-10-612-788-16

28 93 7.7 17 4 US-10-612-788-7 Sequence 7, Appli  
29 83 6.8 338 3 US-09-880-505-32 Sequence 32, Appl  
30 83 6.8 338 3 US-09-880-505-34 Sequence 34, Appl  
31 83 6.8 338 4 US-10-051-643-32 Sequence 32, Appl  
32 83 6.8 338 4 US-10-051-643-34 Sequence 34, Appl  
33 83 6.8 338 4 US-10-329-087-39 Sequence 39, Appl  
34 83 6.8 338 4 US-10-203-562-4 Sequence 4, Appl  
35 83 6.8 338 4 US-10-332-512A-1 Sequence 1, Appl  
36 83 6.8 338 5 US-10-695-155-162 Sequence 162, App  
37 82 6.8 193 4 US-10-612-665-98 Sequence 98, Appl  
38 82 6.8 193 4 US-10-676-694-98 Sequence 98, Appl  
39 82 6.8 419 4 US-10-724-972A-5096 Sequence 5096, Ap  
40 81 6.7 758 4 US-10-408-765A-2652 Sequence 2652, Ap  
41 81 6.7 830 4 US-10-408-765A-2989 Sequence 2989, Ap  
42 81 6.7 970 4 US-10-351-157-135 Sequence 135, App  
43 81 6.7 970 4 US-10-352-554-120 Sequence 120, App  
44 81 6.7 10421 4 US-10-282-122A-61631 Sequence 61631, A  
45 80 6.6 896 4 US-10-408-765A-1811 Sequence 1811, Ap

## ALIGNMENTS

## RESULT 1

US-10-612-788-11

; Sequence 11, Application US/10612788

; Publication No. US20040014947A1

; GENERAL INFORMATION:

; APPLICANT: OGI, Kazuhiro

; APPLICANT: ONDA, Haruo

; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein

; FILE REFERENCE: 2417US1P

; CURRENT APPLICATION NUMBER: US/10/612,788

; CURRENT FILING DATE: 2003-07-02

; PRIOR APPLICATION NUMBER: 09/242,890

; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: PCT/JP97/03194

; PRIOR FILING DATE: 1997-09-10

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 224

; TYPE: PRT

; ORGANISM: human

US-10-612-788-11

Query Match 100.0%; Score 1214; DB 4; Length 224;  
Best Local Similarity 100.0%; Pred. No. 3.6e-117;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSGAVCAPRCPQAPQOQWEGQVMYQSSG 60  
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSGAVCAPRCPQAPQOQWEGQVMYQSSG 60  
Qy 61 RNSRALLSYDGLNORVRVLDERKALIPCKELFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120  
Db 61 RNSRALLSYDGLNORVRVLDERKALIPCKELFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120  
Qy 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT 180  
Db 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT 180  
Qy 181 INYSVILSTRFFDIOLGIKDPSTFTPSTCMAQLEKMSDCSW 224  
Db 181 INYSVILSTRFFDIOLGIKDPSTFTPSTCMAQLEKMSDCSW 224

## RESULT 2

US-10-733-646-2

; Sequence 2, Application US/10733646

; Publication No. US2004012215A1

; GENERAL INFORMATION:

; APPLICANT: Ebner et al.

```
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 1214; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6e-117;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRAPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGRWVYQSSG 60
    |||
DB 1 MPCRAPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGRWVYQSSG 60
    |||

QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||
DB 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPOEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
DB 121 PWDPLDIPONSTPEDQYSIGGPOEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPOEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
DB 121 PWDPLDIPONSTPEDQYSIGGPOEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 181 INYSVILSTRFFDIQLGIKIDPSVFTPPSTCQMAQLEKMSDEDCSW 224
    |||
DB 181 INYSVILSTRFFDIQLGIKIDPSVFTPPSTCQMAQLEKMSDEDCSW 224
    |||

RESULT 3
US-10-733-646-2
; Sequence 2, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 1214; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6e-117;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRAPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGRWVYQSSG 60
    |||
DB 1 MPCRAPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGRWVYQSSG 60
    |||

QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||
DB 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPOEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
DB 121 PWDPLDIPONSTPEDQYSIGGPOEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 181 INYSVILSTRFFDIQLGIKIDPSVFTPPSTCQMAQLEKMSDEDCSW 224
    |||
DB 181 INYSVILSTRFFDIQLGIKIDPSVFTPPSTCQMAQLEKMSDEDCSW 224
    |||

RESULT 5
US-10-733-646-2
; Sequence 1, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417USJP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: human
US-10-612-788-10

Query Match      89.0%; Score 1081; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.9e-103;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGGLCSLGAVGAPRCPQAPQWEGRWVYQSSGRNRRALLSYDGLNQRVRVLDERKA 84
    |||
DB 1 WTLGGLCSLGAVGAPRCPQAPQWEGRWVYQSSGRNRRALLSYDGLNQRVRVLDERKA 60
    |||

QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPONSTPEDQYSIGGPOE 144
    |||
DB 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPONSTPEDQYSIGGPOE 120
    |||

QY 145 QITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFTINYSVILSTRFFDIQLGIKIDPSVF 204
    |||
DB 121 QITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFTINYSVILSTRFFDIQLGIKIDPSVF 180
    |||

QY 205 TPPSTCQMAQLEKMSDEDCSW 224
    |||
DB 181 TPPSTCQMAQLEKMSDEDCSW 200
    |||

RESULT 5
US-10-612-788-1
; Sequence 1, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417USJP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
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Query Match 82.8%; Score 1005; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.3e-95;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 APPCPAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97  
DB 1 APPCPAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60  
QY 98 YKGVNFQIDQATKQCSKMTLTQFMDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKS 157  
DB 61 YKGVNFQIDQATKQCSKMTLTQFMDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKS 120  
QY 158 RSYETWIGYTVKDCYVQETFTINYSVILSTRFFDIQLGKDPSVFTPESTCMAQLEK 217  
DB 121 RSYETWIGYTVKDCYVQETFTINYSVILSTRFFDIQLGKDPSVFTPESTCMAQLEK 180  
QY 218 MSDDCSW 224  
DB 181 MSDDCSW 187

US-10-612-788-1

Query Match 82.8%; Score 1005; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.3e-95;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 APPCPAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97  
DB 1 APPCPAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60  
QY 98 YKGVNFQIDQATKQCSKMTLTQFMDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKS 157  
DB 61 YKGVNFQIDQATKQCSKMTLTQFMDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKS 120  
QY 158 RSYETWIGYTVKDCYVQETFTINYSVILSTRFFDIQLGKDPSVFTPESTCMAQLEK 217  
DB 121 RSYETWIGYTVKDCYVQETFTINYSVILSTRFFDIQLGKDPSVFTPESTCMAQLEK 180  
QY 218 MSDDCSW 224  
DB 181 MSDDCSW 187

## RESULT 6

US-10-612-788-13  
Query Match 82.4%; Score 1000; DB 4; Length 224;  
Best Local Similarity 80.3%; Pred. No. 5.6e-95;  
Matches 179; Conservative 19; Mismatches 25; Indels 0; Gaps 0;  
QY 1 MPCRRLTVPGALGAWLLGGLWNTLCGLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60  
DB 1 MPARAPRLVQGPRTWLLGSLWVWLGLMGAGSLGTTPQCPAPQWEGRQVLYQSSG 60  
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNFQIDQATKQCSKMTLTQ 120  
DB 61 HNNRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNFQIEQATKCAKPLVE 120  
QY 121 PWDPLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYTVKDCYVQETFT 180  
DB 121 SMDPLDIPQNSTFEDQYSIGGPOEQILVQWSDRRTARSYETWIGYTTAKDCYVQETFI 180  
QY 181 INYSVILSTRFFDIQLGKDPSVFTPESTCMAQLEKMSDSCS 223  
DB 181 RNYTVVMSTRFFDVQLGKIDPSVFTPESTCQAAPQWEGRQVLYQSSG 223

## RESULT 7

US-10-612-788-12  
Query Match 81.8%; Score 993; DB 4; Length 224;  
Best Local Similarity 81.8%; Pred. No. 3e-94;  
Matches 180; Conservative 15; Mismatches 25; Indels 0; Gaps 0;  
QY 4 RAPLRTVPGALGAWLLGGLWNTLCGLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNS 63  
DB 4 RAPRRLVQGPRTWLLGSLWVWLGLMGAGSLGTTPQCPAPQWEGRQVLYQSSGSHNS 63  
QY 64 RALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNFQIDQATKQCSKMTLTQPD 123  
DB 64 RALVSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNFQIEQATKCAKPLAE 123  
QY 124 PLDIPQNSTFEDQYSIGGPOEQITVQWSDRKSARSYETWIGYTVKDCYVQETFTINY 183  
DB 124 PLDIPQNSTFEDQYSIGGPOEQILVQWSDRRTARSYETWIGYTTAKDCYVQETFI 183  
QY 184 SVILSTRFFDIQLGKDPSVFTPESTCMAQLEKMSDSCS 223  
DB 184 TVVLSRTRFFDVQLGKIDPSVFTPESTCQAAPQWEGRQVLYQSSG 223

Query Match 81.8%; Score 993; DB 4; Length 224;  
Best Local Similarity 81.8%; Pred. No. 3e-94;  
Matches 180; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

## RESULT 8

US-10-612-788-2  
Query Match 73.5%; Score 892; DB 4; Length 190;  
Best Local Similarity 86.1%; Pred. No. 7.1e-84;  
Matches 161; Conservative 14; Mismatches 12; Indels 0; Gaps 0;  
QY 37 GAPRCPAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYIL 96  
QY 37 GAPRCPAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYIL 96

Query Match 73.5%; Score 892; DB 4; Length 190;  
Best Local Similarity 86.1%; Pred. No. 7.1e-84;  
Matches 161; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Db 3 GTPQCPQAEQWEGRQVLTQSSGHNRSALVSDGLNQVRVLDERKALIPCKRLFYIL 62  
QY 97 LYKDGVMFQIDQATKQCSKMTLTQPDWLDIPQNSTFEDQYSIGGPQEQITVQEWSDRKS 156  
Db 63 LYKDGVMFQIEQATKLCAKIPLAEPWLDIPQNSTFEDQYSIGGPQEQIMVQWSDRRT 122  
QY 157 ARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLE 216  
Db 123 ARSYETWIGYTVKDCYPVQETFTIRNYTVVLSTRFFDVQLGDKPSVFTPPSTCQTAQPE 182  
QY 217 KMSDCS 223  
Db 183 KMKENS 189

RESULT 9  
US-10-612-788-3  
; Sequence 3, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-612-788-3

Query Match 72.1%; Score 875; DB 4; Length 187;  
Best Local Similarity 84.9%; Pred. No. 4e-82;  
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;  
QY 39 PRPCQAPQWEGRQVLYQSSGHNRSALVSDGLNQVRVLDERKALIPCKRLFYILLY 98  
Db 2 PQCQAPQWEGRQVLYQSSGHNRSALVSDGLNQVRVLDERKALIPCKRLFYILLY 61  
QY 99 KDGVMFQIDQATKQCSKMTLTQPDWLDIPQNSTFEDQYSIGGPQEQITVQEWSDRKSAR 158  
Db 62 KEGVMFQIEQATKQCAKIPLESWDLDPQNSTFEDQYSIGGPQEQILVQWSDRTAR 121  
QY 159 SYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLEKX 218  
Db 122 SYETWIGYTVKDCYPVQETFTIRNYTVVLSTRFFDVQLGDKPSVFTPPSTCQAAQPEKX 181  
QY 219 SEDCS 223  
Db 182 SDGCS 186

RESULT 10  
US-10-612-788-14  
; Sequence 14, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: human  
US-10-612-788-14  
Query Match 17.2%; Score 209; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 5.5e-14;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPGRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVG 37  
Db 1 MPGRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVG 37  
RESULT 11  
US-10-612-788-8  
; Sequence 8, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-612-788-8  
Query Match 16.6%; Score 201; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.9e-13;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQVRVLDERKALIPCKRLFYILLYKDGVMFQI 106  
Db 1 SYDGLNQVRVLDERKALIPCKRLFYILLYKDGVMFQI 39

RESULT 12  
US-10-733-646-4  
; Sequence 4, Application US/10733646  
; Publication No. US20040122215A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; FILE REFERENCE: PF403D2  
; CURRENT APPLICATION NUMBER: US/10/733,646  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: US 10/187,904  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 09/229,583  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,330  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: US 60/075,278  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 221

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; TYPE: PRT
; ORGANISM: Oncomorphynchus mykiss
US-10-733-646-4

Query Match      15.9%; Score 192.5; DB 4; Length 221;
Best Local Similarity 25.0%; Pred. No. 2.9e-11;
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

QY 25 WTLGCLSLGAVGAPRCPQAPQWEGRGVVMYQQSSGRNSRALLSYDGLNORVRVLDERKA 84
DB 12 WLCGLGATALESHPQCHTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRFTSEMH 71
QY 85 LIPCKRLFYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGG--- 141
DB 72 LNKTEHLEDYLMUFEEGVFDIDMKQSCCKMSLSHAHALELPAGAAHQVELFLGSDTV 131
QY 142 PQSQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFTTINYSVILSTRFFDIQLGKDP 201
DB 132 QEDNIKVINWVG-SVAETKGQYSALTTVGECPL-STFYSTDSTITLLFSNSVVEVTKAP 189
QY 202 SVETPPSTCQMAQLEK 217
DB 190 EMFTLPSCFAVELEE 205
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RESULT 13
US-10-733-646-4
; Sequence 4, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorphynchus mykiss
US-10-733-646-4

Query Match      15.9%; Score 192.5; DB 5; Length 221;
Best Local Similarity 25.0%; Pred. No. 2.9e-11;
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

QY 25 WTLGCLSLGAVGAPRCPQAPQWEGRGVVMYQQSSGRNSRALLSYDGLNORVRVLDERKA 84
DB 12 WLCGLGATALESHPQCHTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRFTSEMH 71
QY 85 LIPCKRLFYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGG--- 141
DB 72 LNKTEHLEDYLMUFEEGVFDIDMKQSCCKMSLSHAHALELPAGAAHQVELFLGSDTV 131
QY 142 PQSQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFTTINYSVILSTRFFDIQLGKDP 201
DB 132 QEDNIKVINWVG-SVAETKGQYSALTTVGECPL-STFYSTDSTITLLFSNSVVEVTKAP 189
QY 202 SVETPPSTCQMAQLEK 217
DB 190 EMFTLPSCFAVELEE 205
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RESULT 14

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US-10-612-788-5
; Sequence 5, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-5
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Query Match      14.4%; Score 175; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 136
DB 1 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 32
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RESULT 15
US-10-733-646-5
; Sequence 5, Application US/10733646
; Publication No. US20040122215A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Cyprinus carpio
US-10-733-646-5
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Query Match      13.8%; Score 167.5; DB 4; Length 215;
Best Local Similarity 24.4%; Pred. No. 1.1e-08;
Matches 50; Conservative 47; Mismatches 89; Indels 19; Gaps 8;

QY 30 LCSLGAVGAPR-PCQAPQWEGRGVVMYQQSSGRNSRAL--LSYDGLNORVRVLDERKALI 86
DB 14 LCVAWASSNRQPCCHSPPLTSG--TMKVSTGHDHSLASGEFSYDSKANKRFFVEDTAHAN 71
QY 87 PCKRLFYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGP---Q 143
DB 72 KTSHM-DVLVHFEFEGVLYEIDSKNESCKETLQPRKHLMEIPPDATHESBIYMGSPSITE 130
QY 144 EQITVQWSDR-----KSARSYETWIGIYTVKDCYPVOETFTTINYSVILSTRFFDIQLGK 199
DB 131 QGLRVVWNGKLPHELHAHYSLSLST-----TSCGLPVSQSGYDGKDKLLFS--FFGVETEVD 184
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Qy 200 DPSVFTTPTCQMAQLEKMSDCSW 224  
Db 185 DPQVFVPPAYCEAVAFEEAPDDHSF 209

Search completed: June 10, 2006, 03:01:42  
Job time : 186 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 10, 2006, 02:58:49 ; Search time 16 Seconds  
(without alignments)  
177.005 Million cell updates/sec

Title: US-10-733-646-2  
Perfect score: 1214  
Sequence: 1 MPCRAPLRTVFGALWLLG.....TPPSTCOMAQLKMSDCSW 224

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pbp.\*  
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5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pbp.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pbp.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pbp.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	7.2	931	6 US-10-524-979-2	Sequence 2, Appli
2	75.5	6.2	164	7 US-11-293-697-2800	Sequence 2800, Ap
3	74	6.1	1456	6 US-10-505-928-69	Sequence 69, Appl
4	72.5	6.0	790	7 US-11-318-939-13	Sequence 13, Appl
5	69.5	5.7	413	6 US-10-953-349-2422	Sequence 24222, A
6	69.5	5.7	429	6 US-10-953-349-24221	Sequence 24221, A
7	69.5	5.7	431	6 US-10-953-349-24220	Sequence 24220, A
8	69.5	5.7	3882	6 US-10-953-349-5549	Sequence 5549, Ap
9	69.5	5.7	3978	6 US-10-953-349-5548	Sequence 5548, Ap
10	69.5	5.7	4118	6 US-10-953-349-5547	Sequence 5547, Ap
11	69	5.7	193	7 US-11-183-218-16	Sequence 16, Appl
12	69	5.7	802	7 US-11-293-697-3610	Sequence 3610, Ap
13	67.5	5.6	294	6 US-10-953-349-5105	Sequence 5105, Ap
14	67.5	5.6	383	6 US-10-953-349-5104	Sequence 5104, Ap
15	67.5	5.6	439	6 US-10-953-349-5103	Sequence 5103, Ap
16	67.5	5.6	585	7 US-11-233-697-4164	Sequence 4164, Ap
17	66	5.4	184	6 US-10-953-349-28907	Sequence 28907, A
18	66	5.4	204	6 US-10-953-349-28906	Sequence 28906, A
19	66	5.4	272	6 US-10-953-349-28905	Sequence 28905, A
20	66	5.4	730	6 US-10-505-928-841	Sequence 841, App
21	65.5	5.4	371	6 US-10-953-349-11789	Sequence 11789, A
22	65.5	5.4	404	6 US-10-953-349-11788	Sequence 11788, A
23	65.5	5.4	409	6 US-10-953-349-11787	Sequence 11787, A
24	65.5	5.4	1871	6 US-10-501-834-26	Sequence 26, Appl
25	65	5.4	695	7 US-11-293-697-4190	Sequence 4190, Ap

26	64.5	5.3	911	7 US-11-313-450-25	Sequence 25, Appl
27	64	5.3	111	6 US-10-953-349-30150	Sequence 30150, A
28	64	5.3	274	7 US-11-293-697-4076	Sequence 4076, Ap
29	64	5.3	362	7 US-11-293-697-2645	Sequence 2645, Ap
30	63.5	5.2	333	6 US-10-953-349-28481	Sequence 28481, A
31	63.5	5.2	337	6 US-10-953-349-28480	Sequence 28480, A
32	63.5	5.2	345	6 US-10-953-349-28479	Sequence 28479, A
33	63.5	5.2	453	6 US-10-471-571A-1056	Sequence 1056, Ap
34	63.5	5.2	524	7 US-11-293-697-3442	Sequence 3442, Ap
35	63	5.2	174	6 US-10-953-349-4320	Sequence 4320, Ap
36	63	5.2	201	6 US-10-196-749-108	Sequence 108, App
37	63	5.2	277	6 US-10-953-349-4319	Sequence 4319, Ap
38	63	5.2	286	6 US-10-953-349-4318	Sequence 4318, Ap
39	63	5.2	639	7 US-11-293-697-3425	Sequence 3425, Ap
40	63	5.2	847	6 US-10-505-928-495	Sequence 495, App
41	62.5	5.1	208	6 US-10-953-349-30987	Sequence 30987, A
42	62.5	5.1	244	6 US-10-953-349-30986	Sequence 30986, A
43	62.5	5.1	293	6 US-10-953-349-19396	Sequence 19396, A
44	62.5	5.1	324	6 US-10-953-349-19395	Sequence 19395, A
45	62.5	5.1	359	6 US-10-953-349-19394	Sequence 19394, A

ALIGNMENTS

RESULT 1  
US-10-524-979-2  
; Sequence 2, Application US/10524979  
; Publication No. US20060094013A1  
; GENERAL INFORMATION:  
; APPLICANT: Takemori, Hiroshi  
; APPLICANT: Okamoto, Mitsuhiro  
; TITLE OF INVENTION: SALT-INDUCIBLE KINASE 2 AND USE THEREOF  
; FILE REFERENCE: WATA-003  
; CURRENT APPLICATION NUMBER: US/10/524,979  
; CURRENT FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: 2002-240092  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: 2003-23295  
; PRIOR FILING DATE: 2003-01-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 931  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-524-979-2

Query Match	7.2%	Score 88;	DB 6;	Length 931;
Best Local Similarity	23.3%	Pred. No. 0.38;		
Matches	59;	Conservative	34;	Mismatches 80; Indels 80; Gaps 15;
Qy	37	GAPPCQAPQWEGRQ-----VNYQSSGRNSRALLSYDG-----LNQVRV 78		
Db	178	GSP-PYAAPSEVFEGQVGEGLDIWSMGVLYLVLCG-----ALPFDGPTLPILRQRYL- 230		
Qy	79	LDERKALIP-----CKRLFYILLYKGVWFQIDQATKOCCKMTLTQPWD-PLDIPONS 131		
Db	231	--EGRFIPYFMSEDCHELRMLDLDPKRLSLAQ-IKEHKWMLIEVPVQRPILYPOEQ 287		
Qy	132	TFEDQVSGIGGPQEQ-----ITVQWSDRSARSYETWIGIYTV-----KDCYP 174		
Db	288	--ENEPSIGFNEQVLRMHSLGIDQKTVESLQNKSNYHFAIYFLVLVERLKHRSFPP 345		
Qy	175	VQETP-----TINYSVILSTRFFDIQIGKIDPSV-----FT-PPST 209		
Db	346	VEORLDGRQRPSTIAEQTVAKAQTVGLPVLTHPPVRLMRSTLLPOASNVEAFSFTSS 405		
Qy	210	COMAQLEKMSDC 222		
Db	406	CQ-AEAAFMEEEC 417		

RESULT 2  
US-11-293-697-2800  
; Sequence 2800, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2800  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-2800

Query Match 6.2%; Score 75.5; DB 7; Length 164;  
Best Local Similarity 37.7%; Pred. No. 0.83;  
Matches 20; Conservative 5; Mismatches 27; Indels 1; Gaps 1;

QY 5 APLRTVPGALGAWLLGGLWAWTLCGLC-SLGAVGAPRPCAPQOWEGRQVMYQ 56  
Db 46 AGLRPPGSHSVMLPGGLCCRSLSPLCLYLCLLPSRPASWPGIWQGWETPLQ 98

RESULT 3  
US-10-505-928-69  
; Sequence 69, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: Patentin 3.2  
; SEQ ID NO 69  
; LENGTH: 1456  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-69

Query Match 6.1%; Score 74; DB 6; Length 1456;  
Best Local Similarity 23.1%; Pred. No. 18;  
Matches 43; Conservative 23; Mismatches 58; Indels 62; Gaps 12;

QY 1 MPCRAPLRTVPG--ALGAWLLGGLW-----AWTLGGLCSLGAVGAPRPC-----OAP 45  
Db 593 MPRK-----PGCVARTGTAGGLWDLVKDEKAKFVKHNAEGVTHPPKPTTTPPKCP 647  
QY 46 QOWEGRQVMYQOQSSGRNSRALLSY----DGLNQRVRLDERKALIPCKRLFEYILLYKDG 101  
Db 648 EDW-----GASSRTSLCFKLYAKGKHEKKTWFESRDF--CRAL-----GG 685  
QY 102 VMFQIQOATKQCKMTLTQPDWDLDPQNSTPDDQY-----SIGGPOEQITVQWSDRKA 157  
Db 686 DLASINKEEQQTIRWL-----ITASGSYHKLFWLGLTYGSPSEGFT---WSD-GSP 733  
QY 158 RSYETW 163  
Db 734 VSIENW 739

RESULT 4  
US-11-318-939-13  
; Sequence 13, Application US/11318939

; Publication No. US20060099671A1  
; GENERAL INFORMATION:  
; APPLICANT: Sofi, Gerald  
; APPLICANT: Gately, Stephen T.  
; APPLICANT: Twardowski, Przemyslaw  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN  
; FILE REFERENCE: 4228-1-1-1  
; CURRENT APPLICATION NUMBER: US/11/318,939  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/09/500,397  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-11-318-939-13

Query Match 6.0%; Score 72.5; DB 7; Length 790;  
Best Local Similarity 20.1%; Pred. No. 12;  
Matches 51; Conservative 22; Mismatches 98; Indels 83; Gaps 12;

QY 25 WTLGGLCSLGAVGAPRPCAPQOWEGRQVMYQOQSSGRNSRALLSYDGLN---QRVRLDE 81  
Db 235 WEFCDI-----PR-CTTPPTSGTYQCLKGRGENYRGTVSVTASGHTCQRWSAQSP 285  
QY 82 RK-----ALIPCKRLFEYILLYKDGVMFOIDQATKQCKMTLTQPDWDLDP---QNSTF 133  
Db 286 HKHNRTPEFPCKNLEENYCRNPDG-----ETAPWCYTTDSVRVMDYCKIPSCGSSTTS 339  
QY 134 EQQYSIGGPOEQITVQWSDRKSARSY-----ETWIGIYTVKDCYPVQET-- 178  
Db 340 TEHLDAPVPEQTPVAQDCYRGNGESYRGTSSTTITGRKQCSWVSMTPHRR-----EKTGP 395  
QY 179 -----FTINYSVILSTREFDIQLGIKDPVSFTF-----PS 208  
Db 396 NFPNAGLTWNY-----CRNPAD---KSPWCYTTDRVRWEYCNLKKCSETEQOVTFPA 447  
QY 209 TCQMAQLEKXVSEDC 222  
Db 448 IAQVPSVEDLSDC 461

RESULT 5  
US-10-953-349-24222  
; Sequence 24222, Application US/109533349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 24222  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-24222

Query Match 5.7%; Score 69.5; DB 6; Length 413;  
Best Local Similarity 21.1%; Pred. No. 11;  
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;







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; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3610
; LENGTH: 802
; TYPE: prt
; ORGANISM: Homo sapiens
; US-11-293-697-3610

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Query Match      5.7%; Score 69; DB 7; Length 802;
Best Local Similarity 29.1%; Pred.No. 28;
Matches 30; Conservative 9; Mismatches 38; Indels 26; Gaps 5;

QY 128 PQNSTFEDQYS-----IGGP-QSQITVQVMSDRKARSYSYTWIGIYTVKDCYPVQE 177
      | | | | | : | | | | | : | | | | | : |
Db 461 PSTATTSQDLTPSSATFPDPLTSLPQGLT-----ETSVRSYED-----QLTPC----- 504

QY 178 TTFINKSVILSTRFFDQLGKIDPSVTPPSTCMAQLKMS 220

Db 505 TSFTFPDQLLESTATFPFPLGSPAHEOILTPPSTAFQALHDGPSO 547
      | | | | | : | | | | | : | | | | | : |

```

```

RESULT 13
US-10-953-349-5105
; Sequence 5105, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al
; TITLE OF INVENTION: SEQUENCE-DETERMIN
; METHOD FOR IDENTIFYING ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5105
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5105

```

Query Match	5.6%;	Score 67.5;	DB 6;	Length 294;
Best Local Similarity	19.4%;	Pred. No. 11;		
Matches	38;	Conservative 28;	Mismatches 57;	Indels 73; Gaps 9;
Qy	52	QVMYQSSGSRNALLSYDGI	---NORVRVLDERKALIPCKRLFEVILLVK	----- 99
Db	46	KVMGESSMTEARELLLASALEHSDHNR	FVLLSDR-----CAPLYDFGYIKYLLSSPRS	100
Qy	100	-----	-----DGVMFOI-DOATKQC	113
Db	101	FVDSFLTKETRYSVKMSPIPEEKWRKGSOWIALIRSHA	EVIVNDGIVFPVFEKFCRC	160
Qy	114	SKMTLTQWPBPLDIPONSTFEDQYSGGPOE	QITVQWSDRKSAR--SYETW--IGI-YT	168
Db	161	PPIGCTEAWFLFKQRRNCIPDEHY	---QTLTLNQGLESEMERRTVITYVNVN	SGIKYE 217
Qy	169	VKDCCYPVQETFTINYS	184	
Db	218	AKSWHPV--TFTILENS	231	

RESULT 14  
US-10-953-349-5104  
; Sequence 5104, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al  
; TITLE OF INVENTION: SEQUENCE-DETERMIN  
; TITLE OF INVENTION: ENCODED THERBY

```

; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5104
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5104

```

Query Match	5.6%	Score	67.5	DB	6	Length	383
Best Local Similarity	19.4%	Pred. No.	16				
Matches	38	Conservative	28	Mismatches	57	Indels	73
Gaps	9						
Qy	52	QVMYQSSGSRNALLSYDGL	---	NORVRVLDKRALIPCKRLFEVILLYK	-----	99	
		: : : : : :		: : : : : :			
Db	135	KVMWGESSMIEAERLLLASALEDSHQRFVLLSDR	----	CAPLYDFGIYKYLIISSPRS	189		
Qy	100	-----		DGVMFOI-DOATKQC	113		
				: : : : : :			
Db	190	FVDSFLTKETRYSVKMSVPVPEBKMRKGSQWIALIRSHAENVYNDGIVFPVFKEFCRCR	249				
Qy	114	SKMTLTQWPDLDPONSTFEDQVSGCGPQEQITVQWSDRKSAR	--SYETW--	IGI-YT	168		
		: : : : : :		: : : : : :			
Db	250	PLPGTWEAWFLQKRRNCIPDEHYV	---QTLT	TMQGLESEMERVTVYTVVNWSGTKYE	306		
Qy	169	VKDCYPVQETFTINYS	184				
		_ : : : : :					
Db	307	AKSWHPV--TFTLENS	320				

```

RESULT 15
US-10-953-349-5103
; Sequence 5103, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al
; TITLE OF INVENTION: SEQUENCE-DETERMIN
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5103
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5103

```

Query Match	5.6%	Score 67.5;	DB 6;	Length 439;
Best Local Similarity	19.4%;	Pred. No. 19;		
Matches	38; Conservative	28; Mismatches	57; Indels	73; Gaps
Qy	52 QVMYQOSSGRNSRALLSYDGL-----NORVAVLDERKALIPCKRLFEVILLYK-----	99		
Db	191 KVMWGESSMTEARLLLSALEDHNRQFVLLSDR-----CAPLYDFGYIKYLIISSPRS	245		
Qy	100 -----DGUMFOI-QOATKQC	113		
Db	246 FVDSFLHTKETRYSVKMSPVPEEKWRKGSQWIALIRSHAENVINDGIVFPVFKEFCRC	305		
Qy	114 SKMTLTQPMDLPIDPNSTFEDQYSIGGGPOEQTIVQESWDKSAR--SYETW--IGI-YT	168		
Db	306 PPLGTNEAWLFQKQRNCIPDEHYV---QTLITMQGLESEMERERTVTYYTNVWSGTXYE	362		
Qy	169 VKDCYPVOETFTINYS	184		
Db	363 AKSWHPV--TFTLENS	376		

Search completed: June 10, 2006, 03:02:05

Job time : 17 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 03:01:59 ; Search time 199 Seconds  
(without alignments)  
429.646 Million cell updates/sec

Title: US-10-733-646-2\_COPY\_38\_224

Perfect score: 1005  
Sequence: 1 APRPCAPQWEGRQVMYQQ.....TPPSTCQMAQLEKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*
- 10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	100.0	224	2	AAW51119 Human epe
2	1005	100.0	224	2	AAW51119 Human epe
3	1005	100.0	224	3	AAW51119 Human epe
4	1005	100.0	344	9	ADY18068 PRO polyp
5	886	88.2	224	2	AAW51120 Rat epend
6	875	87.1	224	2	AAW51121 Mouse epe
7	875	87.1	224	3	AAW51121 Mouse epe
8	281	28.0	210	6	ABR40123 Human cel
9	84.5	8.4	931	8	ADL72200 Mouse sal
10	84	8.4	426	4	AAW51121 Mouse epe
11	82.5	8.2	1572	5	ABP65360 Bifidobac
12	82	8.2	419	5	ABP39813 Staphyloc
13	82	8.2	419	8	ADS05801 Staphyloc
14	81	8.1	970	7	ADD68250 Murine OS
15	81	8.1	970	7	ADL72200 Mouse sal
16	81	8.1	970	9	AED01101 Mouse onc
17	79.5	7.9	996	9	ADY39977 HIV Pol p
18	79.5	7.9	2548	2	AAW51121 Mouse epe
19	79.5	7.9	2548	7	ADE55538 Human Pro
20	79	7.9	144	6	ABU43346 Protein e
21	79	7.9	611	3	AAG41475 Arabidops
22	78	7.8	1541	8	ADL91598 Yeast rap
23	77	7.7	469	7	ADG63082 Mouse per

ALIGNMENTS

RESULT 1

AAW51119  
ID AAW51119 standard; protein; 224 AA.

XX AC AAW51119;

DT 06-NOV-1998 (first entry)

XX Human endymmin-like protein.

DE Human endymmin-like protein; prophylactic agent; Alzheimer's disease;

XX Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;

XX dementia; cerebellar degeneration; central nervous system; gliocyte;

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..37 /note= "Signal peptide; This sequence is claimed by the

FT Peptide 25..37 inventors under claim 10 in the specification"

FT Peptide /note= "This sequence represents another signal peptide

FT Protein which is part of the precursor protein (residues 25-224)

FT Protein ; the precursor protein claimed by the inventors under

FT Protein claim 9 in the specification"

FT Protein /note= "Human endymmin-like protein; This sequence is

FT Protein claimed by the inventors under claim 2 in the

FT Protein specification"

XX WO9811130-A2.

XX 19-MAR-1998.

PD 10-SEP-1997; 97WO-JP003194.

PR 11-SEP-1996; 96JP-00240880.

PR 28-NOV-1996; 96JP-00318049.

PR 27-MAY-1997; 97JP-00135633.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Ogi K, Onda H;

XX WPI; 1998-250952/22.

DR N-PSDB; AAV07200.

XX New isolated endpendymin-like protein - used to develop products for

PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia

PT or cerebellar degeneration.

XX

XX

PS Claim 2, 9, 10; Fig 1A-1D; 147pp; English.

XX

CC The present sequence represents the human endpendymin-like protein. The

CC invention also claims for the rat endpendymin-like protein (AAWS1120) and

CC its corresponding cDNA (AAV07201), and the mouse endpendymin-like protein

CC (AAWS1121) and its corresponding cDNA (AAV07202). The endpendymin-like

CC proteins of the invention are claimed to have nerve-extending activity,

CC neuro-regenerative activity in the central nervous system, gliocyte

CC stimulating activity or memory forming activity. These endpendymin-like

CC proteins and the corresponding DNA sequences which encode them are also

CC claimed to be useful as therapeutic or prophylactic agents for

CC Alzheimer's disease, Parkinson's disease, Huntington's disease,

CC anyotrophic lateral sclerosis, dementia or cerebellar degeneration

XX

XX Sequence 224 AA;

Query Match 100.0%; Score 1005; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 2.1e-103;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRCPAQWEGRWYQSSGRNSRALLSYDGLNQRVRVLDERKALIPCKRLFYILL 60

|||||

Db 38 APRCPAQWEGRWYQSSGRNSRALLSYDGLNQRVRVLDERKALIPCKRLFYILL 97

|||||

QY 61 YKGVNFQIDQATKQCKMTLTQWDPDLIPQNSTFEDQYSIGGPOEITVQWSDRKA 120

|||||

Db 98 YKGVNFQIDQATKQCKMTLTQWDPDLIPQNSTFEDQYSIGGPOEITVQWSDRKA 157

|||||

QY 121 RSYETWIGITVDCVPQVETFTINYSVLSTRFFDIQLGKIDPSVTFPTTCMAQLEK 180

|||||

Db 158 RSYETWIGITVDCVPQVETFTINYSVLSTRFFDIQLGKIDPSVTFPTTCMAQLEK 217

|||||

QY 181 MSEDSCSW 187

|||||

Db 218 MSEDSCSW 224

|||||

RESULT 2

AAV06511

ID AAY06511 standard; protein; 224 AA.

XX

XX AAY06511;

XX

DT 08-OCT-1999 (first entry)

XX

DE Human endpendymin.

XX

XX Endpendymin; human; Parkinson's disease; Alzheimer's disease; epilepsy;

XX anyotrophic lateral sclerosis; pain; stroke; depression; anxiety;

KW neurological disorder; psychiatric disorder; cancer; therapy; diagnosis.

XX

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT Peptide 1..37 "signal peptide"

FT Domain 18..28

FT /label= CD-I

FT /notes= "conserved domain 1"

FT Protein 38..224

FT /notes= "mature protein"

FT Domain 38..47

FT /label= CD-II

FT /notes= "conserved domain 2"

FT Peptide 45..53

FT /notes= "epitope"

FT Peptide 56..64

FT

FT Domain /note= "epitope"

FT 68..77

FT /label= CD-III

FT /note= "conserved domain 3"

FT Domain 101..107

FT /label= CD-IV

FT /note= "conserved domain 4"

FT Peptide 106..114

FT /note= "epitope"

FT Domain 113..119

FT /label= CD-V

FT /note= "conserved domain 5"

FT Peptide 123..144

FT /note= "epitope"

FT Domain 125..142

FT /label= CD-VI

FT /note= "conserved domain 6"

FT Modified-site 130

FT /note= "N-glycosylated"

FT Domain 143..154

FT /label= CD-VII

FT /note= "conserved domain 7"

FT Peptide 150..160

FT /note= "epitope"

FT Domain 166..180

FT /label= CD-VIII

FT /note= "conserved domain 8"

FT Peptide 168..176

FT /note= "epitope"

FT Modified-site 182

FT /note= "N-glycosylated"

FT Domain 187..193

FT /label= CD-IX

FT /note= "conserved domain 9"

FT Peptide 196..204

FT /note= "epitope"

FT Domain 199..221

FT /label= CD-X

FT /note= "conserved domain 10"

FT Peptide 215..223

FT /note= "epitope"

XX

XX WO936565-A1.

XX

XX 22-JUL-1999.

XX

XX 13-JAN-1999; 99WO-US000818.

XX

XX 14-JAN-1998; 98US-0071330P.

PR 19-FEB-1998; 98US-0075278P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

XX Ruben SM, Ebner R;

XX

XX WPI; 1999-458471/38.

DR N-PSDB; AAX87343.

XX

XX A novel human endpendymin and related nucleic acids, useful for treating

XX and diagnosis of nervous system-related disorders.

XX

XX Claim 1; Page 76-77; 90pp; English.

XX

CC This sequence represents human endpendymin, a novel member of the endpendymin

CC family. It was deduced from a cDNA clone (see AAX87343) discovered in a

CC primary dendritic cell cDNA library. Additional clones have been obtained

CC from KWH2, placenta, foetal and adult liver, spinal core, osteoclastoma,

CC cerebellum, synovial fibroblast, 12-week human embryo, adrenal gland

CC tumour, whole brain, Hodgkin's lymphoma, macrophage, HSL cell and

CC chondrosarcoma cDNA libraries. Endpendymin polynucleotides, polypeptides

CC (including the full-length or mature polypeptide, epitope-bearing

CC polypeptides, and modified endpendymin), vectors and host cells are

CC provided, as well as methods for identifying agonists and antagonists of

CC ependymin activity. Human ependymin can be used to treat conditions in  
CC patients having need of the ependymin protein. Conditions that can be  
CC treated or detected are nervous system-related disorders, such as  
CC Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis,  
CC pain, stroke, depression, anxiety, epilepsy and other neurological or  
CC psychiatric disorders. Diagnosis of cancers of the nervous system is also  
CC included. Ependymin, or its agonists or antagonists may also be used to  
CC treat disorders of the blood-brain barrier since ependymin participates  
CC in the endothelial cell barrier by modulating cell-matrix interactions.  
CC Antagonists may inhibit formation of ependymin-collagen fibrils, which  
CC cover endothelial cells of numerous blood vessels, hence anti-ependymin  
CC antibodies may regulate angiogenesis  
XX

SQ Sequence 224 AA;

Query Match 100.0%; Score 1005; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 2.1e-103;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGVQWYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 60  
DB 38 APRPCAPQWEGVQWYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 97  
QY 61 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKA 120  
DB 98 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKA 157  
QY 121 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFDFIQLGKDPSPVTPPSTCMAQLEK 180  
DB 158 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFDFIQLGKDPSPVTPPSTCMAQLEK 217  
QY 181 MSEDCSW 187  
DB 218 MSEDCSW 224

## RESULT 3

AAY94654  
ID AAY94654 standard; protein; 224 AA.

AC AAY94654;

DT 29-AUG-2000 (first entry)

XX Human homology to ependymin-like protein (HELP) amino acid sequence.

XX Homology to ependymin-like protein; HELP; chromosome 7p14-12;  
KW central nervous system disorder; peripheral nervous system disorder;  
KW Alzheimer's disease; memory loss; stroke; neuronal damage;  
KW osteoblast differentiation; proliferation; stimulation; bone wear;  
KW arthritis; osteoporosis; cerebral cavernous malformation;  
KW Charcot-Marie-Tooth syndrome; human; netrin like protein; NEL.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Peptide 1..37

FT /label= Putative signal peptide

FT Protein 38..224

FT /label= Homology to ependymin-like protein

XX WO200032746-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028341.

XX 30-NOV-1998; 98US-00201442.

XX (MILL-) MILLENNIUM PHARM INC.

XX Pan Y;

XX

DR WPI; 2000-412299/35.  
XX N-PSDB; AAA27982.

XX New nucleic acid molecules, designated NEL, useful for treating  
PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and  
PT neuronal damage (e.g. stroke).

XX Claim 9; Fig 4; 97pp; English.

XX This sequence represents a human homology to ependymin-like protein  
CC (HELP) amino acid sequence. Ependymin is a protein that is involved in  
CC memory and neuronal regeneration. The human HELP gene is located on  
CC chromosome 7p14-12. Northern analysis of HELP expression showed that an  
CC approximately 3kB HELP transcript is expressed in the brain, heart, and  
CC skeletal muscle. HELP is a secreted protein. Modulators of HELP  
CC expression or activity can be used to treat disorders of the central  
CC nervous system or peripheral nervous system, e.g. neuronal disorders,  
CC memory associated disorders, such as Alzheimer's disease or stroke, or to  
CC treat neuronal damage. HELP polypeptides, nucleic acids and modulators of  
CC HELP expression or activity may be useful for modulation of osteoblast  
CC differentiation, stimulation or proliferation. They may also be used to  
CC treat cartilage or bone wearing, arthritis or osteoporosis, disorders  
CC such as cerebral cavernous malformation and Charcot-Marie-Tooth disease.  
CC The present invention also relates to a secreted protein with homology to  
CC netrin, called netrin like protein or NEL. NEL is also referred to as  
CC TANGO 205 or T205. Netrin is a chemoattractant. Biological activities of  
CC NEL include interacting with the protein encoded by deleted in colorectal  
CC cancer, modulation of axon growth, migration and development, modulation  
CC of development of the nervous system, and modulation of the guidance of  
CC central nervous system commissural axons and peripheral motor axons  
XX

SQ Sequence 224 AA;

Query Match 100.0%; Score 1005; DB 3; Length 224;

Best Local Similarity 100.0%; Pred. No. 2.1e-103;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGVQWYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 60  
DB 38 APRPCAPQWEGVQWYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 97  
QY 61 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKA 120  
DB 98 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKA 157  
QY 121 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFDFIQLGKDPSPVTPPSTCMAQLEK 180  
DB 158 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFDFIQLGKDPSPVTPPSTCMAQLEK 217  
QY 181 MSEDCSW 187  
DB 218 MSEDCSW 224

## RESULT 4

ADY18068

ID ADY18068 standard; protein; 344 AA.

AC ADY18068;

XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 3874.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

```
XX 24-FEB-2005.
XX
XX PD
XX PF 11-AUG-2004; 2004WO-US026249.
XX
XX PR 11-AUG-2003; 2003US-0493546P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX
XX WPI; 2005-102330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 3874; 150pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.
XX
XX Sequence 344 AA;
XX
Query Match 100.0%; Score 1005; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.8e-103;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 APRCPAQWEGRQVNYQSSGRNRSALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
Db 150 APRCPAQWEGRQVNYQSSGRNRSALLSYDGLNQRVRLDERKALIPCKRLFEYILL 217
XX
QY 61 YKGVNMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKA 120
Db 218 YKGVNMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKA 277
XX
QY 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSVFTPPSTCQMAQLEK 180
Db 278 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSVFTPPSTCQMAQLEK 337
XX
QY 181 MSEDCSW 187
Db 338 MSEDCSW 344
XX
RESULT 5
AAW51120
ID AAW51120 standard; protein; 224 AA.
XX
AC AAW51120;
XX
XX 06-NOV-1998 (first entry)
XX
DE Rat ependymin-like protein.
XX
KW Rat ependymin-like protein; prophylactic agent; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW dementia; cerebellar degeneration; central nervous system; gliocyte;
KW memory; neuron.
XX
OS Rattus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..34
FT /note= "signal peptide; This sequence is claimed by the
FT inventors under claim 10 in the specification"
FT
FT Protein 35..224
FT /note= "Rat ependymin-like protein; This sequence is
FT claimed by the inventors under claim 2 in the
FT specification"
```

```
XX WO9811130-A2.
XX
XX PD 19-MAR-1998.
XX
XX PF 10-SEP-1997; 97WO-JP003194.
XX
XX PR 11-SEP-1996; 96JP-00240880.
XX
XX PR 28-NOV-1996; 96JP-00318049.
XX
XX PR 27-MAY-1997; 97JP-00135633.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Ogi K, Onda H;
XX
XX WPI; 1998-250952/22.
XX
XX N-PSDB; AAV07201.
XX
XX New isolated ependymin-like protein - used to develop products for
PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia
PT or cerebellar degeneration.
XX
XX Claim 2, 9, 10; Fig 2A-2C; 147pp; English.
XX
XX The present sequence represents the rat ependymin-like protein. The
CC invention also claims for the human ependymin-like protein (AAW51119) and
CC its corresponding cDNA (AAV07200), and the mouse ependymin-like protein
CC (AAW51121) and its corresponding cDNA (AAV07202). The ependymin-like
CC proteins of the invention are claimed to have nerve-extending activity,
CC neuro-regenerative activity in the central nervous system, gliocyte
CC stimulating activity or memory forming activity. These ependymin-like
CC proteins and the corresponding DNA sequences which encode them are also
CC claimed to be useful as therapeutic or prophylactic agents for
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, dementia or cerebellar degeneration.
XX
XX Sequence 224 AA;
XX
Query Match 88.2%; Score 886; DB 2; Length 224;
Best Local Similarity 86.5%; Pred. No. 4.2e-90;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;
XX
QY 2 PRCPAQWEGRQVNYQSSGRNRSALLSYDGLNQRVRLDERKALIPCKRLFEYILL 61
Db 39 POPCPAQWEGRQVLYQQSSGHNSRALSYDGLNQRVRLDERKALIPCKRLFEYILL 98
XX
QY 62 KGVNMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSAR 121
Db 99 KGVNMFQIRQATKLCAKIPLAEFPWDPDIPQNSTFEDQYSIGGPQEQIMVQWSDRRTAR 159
XX
QY 122 SYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSVFTPPSTCQMAQLEKM 181
Db 159 SYETWIGVYTAKDCYPVQETFTIRNYTVLSTRFFDVQLGKDPSVFTPPSTCQTAQPEKM 218
XX
QY 182 SEDCS 186
Db 219 KENCS 223
XX
RESULT 6
AAW51121
ID AAW51121 standard; protein; 224 AA.
XX
AC AAW51121;
XX
XX 06-NOV-1998 (first entry)
XX
DE Mouse ependymin-like protein.
XX
KW Mouse ependymin-like protein; prophylactic agent; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW dementia; cerebellar degeneration; central nervous system; gliocyte;
KW memory; neuron.
```

XX OS Mus sp.  
XX FH Key  
XX FT Peptide  
XX FT 1...37 Location/Qualifiers  
XX FT /note= "Signal peptide; This sequence is claimed by the  
XX FT inventors under claim 10 in the specification"  
XX FT 38...224  
XX FT /note= "Mouse ependymin-like protein; This sequence is  
XX FT claimed by the inventors under claim 2 in the  
XX FT specification"  
XX PN WO9811130-A2.  
XX XX  
XX PD 19-MAR-1998.  
XX XX  
XX PF 10-SEP-1997; 97WO-JP003194.  
XX XX  
XX PR 11-SEP-1996; 96JP-00240880.  
XX PR 28-NOV-1996; 96JP-00318049.  
XX PR 27-MAY-1997; 97JP-00135633.  
XX XX  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX XX  
XX PI Ogi K, Onda H;  
XX XX  
XX DR WPI; 1998-250952/22.  
XX DR N-PSDB; AAV07202.  
XX XX  
XX PT New isolated ependymin-like protein - used to develop products for  
XX PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia  
XX PT or cerebellar degeneration.  
XX XX  
XX PS Claim 2, 9, 10; Fig 3A-3D; 147pp; English.  
XX XX  
XX CC The present sequence represents the mouse ependymin-like protein. The  
XX CC invention also claims for the rat ependymin-like protein (AAW51120) and  
XX CC its corresponding cDNA (AAV07201), and the human ependymin-like protein  
XX CC (AAW51119) and its corresponding cDNA (AAV07200). The ependymin-like  
XX CC proteins of the invention are claimed to have nerve-extending activity,  
XX CC neuro-regenerative activity in the central nervous system, gliocyte  
XX CC stimulating activity or memory forming activity. These ependymin-like  
XX CC proteins and the corresponding DNA sequences which encode them are also  
XX CC claimed to be useful as therapeutic or prophylactic agents for  
XX CC Alzheimer's disease, Parkinson's disease, Huntington's disease,  
XX CC amyotrophic lateral sclerosis, dementia or cerebellar degeneration  
XX XX  
XX SQ Sequence 224 AA;  
Query Match 87.1%; Score 875; DB 2; Length 224;  
Best Local Similarity 84.9%; Pred. No. 7.1e-89;  
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;  
Qy 2 PRPQAPQWEGRQVMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILLY 61  
Db 39 PQCQAPQWEGRQVLYQQSSGHNRLVSYDGLNQVRVLDERKALIPCKRLFEYILLY 98  
Qy 62 KGVWFQIDQATKQCKMTLTPWDPDIPQNSTFEDQYSIGGQEQITVQWSDRSAR 121  
Db 99 KEGVMFQIEQATKQCAKIPLVESDPLDIPQNSTFEDQYSIGGQEQILVQWSDRRTAR 158  
Qy 122 SYETWIGYTVKDCYPVQETTTINYSVLTSFRFFDIOLGIKDPGVSFTPPSTCQMAQLCKM 181  
Db 159 SYETWIGYTVKDCYPVQETTTINYSVLTSFRFFDIOLGIKDPGVSFTPPSTCQMAQLCKM 218  
Qy 182 SEDCS 186  
Db 219 SDGCS 223  
RESULT 7  
AAV94655  
ID AAV94655 standard; protein; 224 AA.

XX AC AAY94655;  
XX DT 29-AUG-2000 (first entry)  
XX DE Murine homology to ependymin-like protein (HELP) amino acid sequence.  
XX XX  
XX KW Homology to ependymin-like protein; HELP; Alzheimer's disease; stroke;  
XX KW central nervous system disorder; peripheral nervous system disorder; NEL;  
XX KW neuronal damage; memory loss; osteoblast differentiation; proliferation;  
XX KW stimulation; bone wear; arthritis; osteoporosis; netrin like protein;  
XX KW cerebral cavernous malformation; Charcot-Marie-Tooth syndrome; mouse.  
XX OS Mus sp.  
XX XX  
XX FH Key  
XX FT Peptide  
XX FT 1...37 Location/Qualifiers  
XX FT /label= Putative signal peptide  
XX FT 38...224  
XX FT Protein  
XX FT /label= Homology to ependymin-like protein  
XX PN WO200032746-A2.  
XX XX  
XX PD 08-JUN-2000.  
XX XX  
XX PF 30-NOV-1999; 99WO-US028341.  
XX XX  
XX PR 30-NOV-1998; 98US-00201442.  
XX XX  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX XX  
XX PI Pan Y;  
XX XX  
XX DR WPI; 2000-412299/35.  
XX DR N-PSDB; AAA27983.  
XX XX  
XX PT New nucleic acid molecules, designated NEL, useful for treating  
XX PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and  
XX PT neuronal damage (e.g. stroke).  
XX PS Claim 9; Fig 3; 97pp; English.  
XX XX  
XX CC This sequence represents a mouse homology to ependymin-like protein  
XX CC (HELP) amino acid sequence. Ependymin is a protein that is involved in  
XX CC memory and neuronal regeneration. HELP is a secreted protein. Northern  
XX CC analysis of HELP expression showed that an approximately 3kb HELP  
XX CC transcript is expressed in the brain, heart, and skeletal muscle. HELP is  
XX CC expressed in a punctate manner throughout adult mouse brain, suggesting  
XX CC that it is expressed by neurons, it is also expressed in the membrane  
XX CC surrounding the placenta. Modulators of HELP expression or activity can  
XX CC be used to treat disorders of the central nervous system or peripheral  
XX CC nervous system, e.g. neuronal disorders, memory associated disorders,  
XX CC such as Alzheimer's disease or stroke, or to treat neuronal damage. HELP  
XX CC polypeptides, nucleic acids and modulators of HELP expression or activity  
XX CC may be useful for modulation of osteoblast differentiation, stimulation  
XX CC or proliferation. They may also be used to treat cartilage or bone  
XX CC wearing, arthritis or osteoporosis, disorders such as cerebral cavernous  
XX CC malformation and Charcot-Marie-Tooth disease. The present invention also  
XX CC relates to a secreted protein with homology to netrin, called netrin like  
XX CC protein or NEL. NEL is also referred to as TANGO 205 or T205. Netrin is a  
XX CC chemoattractant. Biological activities of NEL include interacting with  
XX CC the protein encoded by deleted in colorectal cancer, modulation of axon  
XX CC growth, migration and development, modulation of development of the  
XX CC nervous system, and modulation of the guidance of central nervous system  
XX CC commissural axons and peripheral motor axons  
XX XX  
XX SQ Sequence 224 AA;  
Query Match 87.1%; Score 875; DB 3; Length 224;  
Best Local Similarity 84.9%; Pred. No. 7.1e-89;  
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;  
Qy 2 PRPQAPQWEGRQVMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILLY 61

Db 39 PQFCQAPQWEGRQVLVYQSSGHNRLVSYDGLNQRVRLDERKALIPCKRLFEVILLY 98  
Qy 62 KDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGGPQBQITVQWSDRSAR 121  
Db 99 KEGVMFQIEQATKQCAKIPLVESWDPDLPDIPQNSTFEDQYSIGGPQBQILVQWSDRRTAR 158  
Qy 122 SYETWIGTYVDCYCPVQETFTTNYSVILSTRFEDTQLGHKDPSTVTPSTCQMAQLEKM 181  
Db 159 SYETWIGVYAKDCYCPVQETFTTNYSVILSTRFEDTQLGHKDPSTVTPSTCQMAQPEKM 218  
Qy 182 SEDCS 186  
Db 219 SDGCS 223  
RESULT 8  
ABR40123  
ID ABR40123 standard; protein; 210 AA.  
XX ABR40123;  
XX  
XX 04-JUL-2003 (first entry)  
DE Human cell adhesion and extracellular matrix protein, CADECM-20.  
DE  
XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;  
KW anticonvulsant; nootropic; neuroprotective; immunosuppressive;  
KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;  
KW gene therapy; cell adhesion; extracellular matrix; CADSCM;  
KW immune system disorder; AIDS; allergy; neurological disorder; stroke;  
KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;  
KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;  
KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;  
KW atherosclerosis.  
XX  
XX Homo sapiens.  
XX  
XX WO2003027230-A2.  
XX  
XX 03-APR-2003.  
XX  
XX 02-AUG-2002; 2002WO-US024649.  
XX  
XX 03-AUG-2001; 2001US-0309964P.  
XX 03-AUG-2001; 2001US-0310119P.  
XX 17-AUG-2001; 2001US-0313091P.  
XX 31-AUG-2001; 2001US-0316771P.  
XX 07-SEP-2001; 2001US-0317896P.  
XX 21-SEP-2001; 2001US-0324781P.  
XX 05-OCT-2001; 2001US-0327606P.  
XX 12-OCT-2001; 2001US-0328960P.  
XX 09-NOV-2001; 2001US-0344471P.  
XX 17-MAY-2002; 2002US-0381291P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;  
PI Forsythe IJ, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;  
PI Kalllick DA, Xu Y, Honcheil CD, Baughn MR, Gietzen KJ, Lee S;  
PI Walia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;  
XX  
XX WPI; 2003-354645/33.  
DR N-PSDB; ACC00411.  
XX  
XX New human cell adhesion and extracellular matrix proteins (CADECM),  
PT useful for diagnosing, treating or preventing disorders associated with  
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies  
PT or stroke.  
XX  
XX Claim 1; Page 203; 234pp; English.  
XX  
XX The present invention relates to novel human cell adhesion and

CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding  
CC sequences (ACC00392-ACC0413 and ABR40104-ABR40125). The coding sequences  
CC and proteins are useful in diagnosing, treating and preventing disorders  
CC associated with aberrant expression of CADECM, such as immune system  
CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,  
CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's  
CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic  
CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell  
CC proliferative disorders (e.g. cancer or atherosclerosis)  
XX  
XX Sequence 210 AA;  
SQ  
Query Match 28.0%; Score 281; DB 6; Length 210;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22; Indels 0; Gaps 0;  
Matches 53; Conservative 0; Mismatches 0;  
QY 1 APRPCAPQWEGRQVYQSSGHNRLVSYDGLNQRVRLDERKALIPCKR 53  
Db 158 APRPCAPQWEGRQVYQSSGHNRLVSYDGLNQRVRLDERKALIPCKR 210  
RESULT 9  
ADL72200  
ID ADL72200 standard; protein; 931 AA.  
XX  
XX ADL72200;  
XX  
XX 20-MAY-2004 (first entry)  
DE Mouse salt-inducible kinase 2 (SIK2) enzyme.  
XX  
XX SIK2; salt-inducible kinase 2; cAMP; antidiabetic; anorectic;  
KW hypotensive; antiarteriosclerotic; mouse; enzyme.  
XX  
XX Mus musculus.  
XX  
XX WO2004018669-A1.  
XX  
XX 04-MAR-2004.  
XX  
XX 20-AUG-2003; 2003WO-JP010535.  
XX  
XX 21-AUG-2002; 2002JP-00240092.  
XX 31-JAN-2003; 2003JP-00023295.  
XX  
XX (PROT-) PROTEIN EXPRESS CO LTD.  
XX (TAKE/) TAKEMORI H.  
XX (OKAM/) OKAMOTO M.  
XX  
XX Takemori H, Okamoto M;  
XX  
XX WPI; 2004-238976/22.  
XX N-PSDB; ADL72199.  
XX  
XX Salt inducible kinases 2 and antibodies against them for treatment of  
PT diabetes, obesity, hypertension, arteriosclerosis, circulatory disorders.  
XX  
XX Claim 1; SEQ ID NO 2; 133pp; Japanese.  
XX  
XX The invention relates to salt-inducible kinase (SIK) 2 polypeptides and  
CC encoding polynucleotides that may control the translation activity of a  
CC gene under the control of a cAMP response sequence. The SIK2 polypeptides  
CC and polynucleotides may be used in medical compositions for treating and  
CC detecting diabetes, obesity, hypertension, arteriosclerosis, circulatory  
CC disorders and high uric acid levels in the blood. The present sequence  
CC represents a mouse salt-inducible kinase 2 polypeptide.  
XX  
XX Sequence 931 AA;  
SQ  
Query Match 8.4%; Score 84.5; DB 8; Length 931;  
Best Local Similarity 22.9%; Pred. No. 13;  
Matches 57; Conservative 33; Mismatches 80; Indels 79; Gaps 14;







CC producing an *S. epidermidis* polypeptide; an isolated nucleic acid  
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
CC vaccine composition for prevention or treatment of an *S. epidermidis*  
CC infection, comprising a nucleic acid cited above and a carrier; treating  
CC a subject for *S. epidermidis* infection; a recombinant or substantially  
CC pure preparation of an *S. epidermidis* polypeptide or its fragment; a  
CC vaccine composition for prevention or treatment of an *S. epidermidis*  
CC infection; detecting the presence of a *Staphylococcus* nucleic acid in a  
CC sample; a computer readable medium having recorded in it the nucleotide  
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
CC system for identifying fragments of the *Staphylococcus* genome of  
CC commercial importance; a computer based system for identifying fragments  
CC of the *Staphylococcus* plasmids of commercial importance; identifying  
CC commercially important nucleic acid fragments of the *Staphylococcus*  
CC genome and/or plasmids; and identifying an expression modulating fragment  
CC of the *Staphylococcus* genome and/or plasmids. The methods and  
CC compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of an *Staphylococcal* epidermidis bacterial  
CC infection. This is the amino acid sequence of a *S. epidermidis* protein of  
CC the invention.  
XX  
SQ Sequence 419 AA;

Query Match 8.2%; Score 82; DB 8; Length 419;  
Best Local Similarity 26.1%; Pred. No. 7.8;  
Matches 42; Conservative 19; Mismatches 60; Indels 40; Gaps 8;  
QY 39 VRVLDERKALIPCKRLFEYLLYKDGVMFOIDQATK-----QCSKMTLQ-----P 84  
D 19 VESLDE-----SLYEIVSQICEEVKLGQDKALKNNYLQFDQVTEKLEQSOLKNA 70  
QY 85 WDLPLDPQNSTFFEDQYS-IGGPQQTITVQWSDRKSARSYETW-----IGYTVV--KDCY 136  
D 71 YDMLDNETRDALQESYQRIKVVYQENIKVQESSQOT-ECYERHPIERVGIYVPGKASY 129  
QY 137 PVQETFTINYSVILSTRFFDIQLGIKDPSTFTTTPSTCMAQ 177  
D 130 P-----STVLMTATLAQVAGVNEITVTPPQNSGICQ 161

RESULT 14  
ADP68250  
ID ADD68250 standard; protein; 970 AA.  
XX  
AC ADD68250;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Murine OSMRbeta polypeptide SEQ ID NO:120.  
XX  
KW mouse; zcytor17; antiinflammatory; dermatological; immunosuppressive;  
KW antimicrobial; vaccine; inflammatory disease; inflammatory bowel disease;  
KW ulcerative colitis; Crohn's disease; atopic dermatitis; eczema;  
KW psoriasis; endotoxaemia; septicemia; toxic shock syndrome;  
KW infectious disease.  
XX  
OS Mus musculus.  
XX  
FN W0203060090-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 21-JAN-2003; 2003WO-US001984.  
XX  
PR 18-JAN-2002; 2002US-0350325P.  
PR 25-APR-2002; 2002US-0375323P.  
PR 19-DEC-2002; 2002US-0435315P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Sprecher CA, Kuijper JL, Dasovich MM, Grant FU, Hammond AK;  
PI Novak JE, Gross JA, Dillon SR;  
XX

DR WPI; 2003-618179/58.  
XX N-PSDB; ADD68249.  
XX  
PT New zcytor17 ligand polypeptides, useful for treating inflammatory  
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's  
PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.  
XX  
PS Example 38; SEQ ID NO 120; 372pp; English.  
XX  
CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A  
CC polypeptide of the invention has antiinflammatory, dermatological,  
CC immunosuppressive, and antimicrobial activity, and may have a use in a  
CC vaccine. The polypeptide is useful for treating inflammatory diseases,  
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
CC shock syndrome or infectious diseases. The present sequence is used in  
CC the exemplification of the invention.  
XX

SQ Sequence 970 AA;

Query Match 8.1%; Score 81; DB 7; Length 970;  
Best Local Similarity 23.7%; Pred. No. 34;  
Matches 33; Conservative 24; Mismatches 60; Indels 22; Gaps 6;  
QY 17 MYQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKD-----GV 65  
D 597 IFERSVEHKARLVEKQRGYQELAPLVNPKVEIPYSTPNSFVLWPDVDSDFQAGFIKGY 656  
QY 66 MFQIDQNTQKCSKMTLTQPDWDLDPONSTFEDQYSIGGPQ-EOITVQWSDRKSARSYE 124  
D 657 LVVYKSKEMQCN-----QPWERTLLPDNSVL-CKYDINGSETKLTVE---NLQPSLSYE 707  
QY 125 TWIGIYTVKDCYPVQETFT 143  
D 708 FVTPYTSAGPGP-NETFT 725

RESULT 15  
ADL26698  
ID ADL26698 standard; protein; 970 AA.  
XX  
AC ADL26698;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Soluble mouse OSMRbeta receptor.  
XX  
KW antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;  
KW antibacterial; immunosuppressive; cell proliferation inhibitor;  
KW immune response inhibitor; inflammatory response inhibitor;  
KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;  
KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;  
KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;  
KW haematopoietic progenitor cell; zcytor17lig-induced inflammation;  
KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;  
KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;  
KW septicemia; toxic shock syndrome; zcytor17lig; zcytor17;  
KW OSMRbeta receptor; receptor; mouse.  
XX  
OS Mus musculus.  
XX  
FN US2003215838-A1.  
XX  
PD 20-NOV-2003.  
XX  
PF 21-JAN-2003; 2003US-00351157.  
XX  
PR 18-JAN-2002; 2002US-0350325P.  
PR 14-JUN-2002; 2002US-0389108P.  
PR 19-DEC-2002; 2002US-0435361P.  
XX  
XX (SPRE/) SPRECHER C A.  
XX (GAOZ/) GAO Z.  
PA



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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:05:54 ; Search time 40 Seconds  
(without alignments)  
449.813 Million cell updates/sec

Title: US-10-733-646-2\_COPY\_38\_224

Perfect score: 1005

Sequence: 1 APRPCAPQWEGRVQVYQ.....TPPSTCQMAQLEKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.5	18.0	221	JC1251	ependymin Om-II pr
2	173.5	17.3	221	JC1250	ependymin Om-I pre
3	172.5	17.2	221	I50538	ependymin - north
4	163	16.2	215	I51377	ependymin precursor
5	162	16.1	212	I50490	ependymin - Atlant
6	152	15.1	216	JU0090	ependymin precursor
7	151	15.0	217	A43820	ependymin precursor
8	148	14.7	216	A32636	ependymin II precu
9	79.5	7.9	2548	E59435	myosin IXA (import
10	79	7.9	257	C97109	specialized DNA-de
11	79	7.9	257	T40621	probable transcrip
12	78.5	7.8	275	A72319	conserved hypothet
13	78	7.8	288	I55184	repA protein - Bsc
14	78	7.8	1085	E70834	probable regulator
15	78	7.8	1541	S46686	hypothetical prote
16	77.5	7.7	643	G64412	hypothetical prote
17	76	7.6	295	T40061	hypothetical prote
18	75.5	7.5	600	E81733	DNA primase TC0175
19	75.5	7.5	685	I64946	oligopeptidase B (
20	74.5	7.4	615	PH0853	methyl-directed mi
21	74.5	7.4	632	S64786	hypothetical prote
22	73.5	7.3	1219	S54570	probable membrane
23	73.5	7.3	1720	T07258	cell division prot
24	73	7.3	1148	T13347	Cnn protein - frui
25	73	7.3	1451	B86286	F91.15 protein -
26	73	7.3	1641	T10955	early nodulin bind
27	72.5	7.2	552	S50313	iron transport pro
28	72.5	7.2	1442	C92898	DNA polymerase III
29	72	7.2	341	F72215	oligopeptide ABC t

ALIGNMENTS

RESULT 1

JC1251

ependymin Om-II precursor - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C:Accession: JC1251

R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.

Gene 118, 189-196, 1992

A:Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and

A:Reference number: JC1250; MUID:92380503; PMID:1511892

A:Accession: JC1251

A:Molecule type: mRNA

A:Residues: 1-221 <MUE>

A:Cross-references: UNIPROT:P28771; UNIPARC:UPI000012A096; GB:M93698; NID:G213413; PID:

C:Comment: This protein shares several characteristics with soluble glycoproteins medi

C:Genetics:

A:Gene: Om-II

C:Superfamily: ependymin

C:Keywords: glycoprotein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-221/Product: ependymin Om-II #status predicted <Mat>

F:33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	18.0%	Score 180.5;	DB 2;	Length 221;
Best Local Similarity	25.3%	Pred. No. 4e-10;	Mismatches 38;	Indels 5; Gaps 3;
Matches	46;	Conservative	93;	
Qy	2	PRPCAPQWEGRVQVYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLY	61	
Db	26	PQCHTSPNMTGLVTMALTGGEIKATGHYSYDSTNKKLRFTESEMHNLKTEHLEDYLMFL	85	
Qy	62	KGVNFQIDQATKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGG---	POEQITVQWSBRK	118
Db	86	EEGVFYDIDMKQSCCKMSLHAHALELPAGAAHQVELFLGSDTVQEDNKKVNTWMG-S	144	
Qy	119	SARSVEWIGYTVKDCVPVQETFTINVSVLTSFRFPDIQLGIDKPSVFTPESTCQMAQL	178	
Db	145	VAETKGQVSALTTVGECUPL--STFYSTDITLLFSNSEVTVTKAPENFTLPSFCEAVEL	203	
Qy	179	EK 180		
Db	204	EE 205		

RESULT 2

JC1250

ependymin Om-I precursor - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C:Accession: JC1250; PCl124

R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.

Gene 118, 189-196, 1992

A;Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and md  
A;Reference number: JCI1250; MUID:92380503; PMID:1511892  
A;Accession: JCI1250  
A;Molecule type: mRNA  
A;Residues: 1-221 <MUE>  
A;Cross-references: UNIPROT:P28770; UNIPARC:UPI000012A092; GB:M93697; NID:g213411; PIDN:  
A;Accession: PCL124  
A;Molecule type: protein  
A;Residues: 22-44;198-221 <MU2>  
A;Cross-references: UNIPARC:UPI00001788FF; UNIPARC:UPI0000178900  
C;Comment: This protein shares several characteristics with soluble glycoproteins mediato  
C;Genetics:  
A;Gene: Om-I  
C;Superfamily: ependymin  
C;Keywords: Glycoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-221/Product: ependymin Om-I #status experimental <MAT>  
F;33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.3%; Score 173.5; DB 2; Length 221;  
Best Local Similarity 24.3%; Pred. No. 1.9e-09;  
Matches 45; Conservative 39; Mismatches 96; Indels 5; Gaps 3;

Qy 2 PRCPQAPQWEGRWVYQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLY 61  
Db 26 PQHCTSPNMTGVLTVMALNGEIKATGHYSDYTDKKIRPTESEMHKTEHLEDYLMLF 85

Qy 62 KDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGG---PQEQITVQWSDRK 118  
Db 86 EGVFYDIDMKNQSKCKWLSHAHALELPAGAHHQVELFLGSDTVQEEIDIKNIWTSV 145

Qy 119 SARYETWIGIYTKQCYVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQL 178  
Db 146 PETKGQVFLST-TVGECLPL-STFYSTDSTITLFSNSQVTEVKAPVFNLPSCGVEL 203

Qy 179 EKMS 183  
Db 204 EEAPE 208

RESULT 3  
150538  
ependymin - northern pike  
C;Species: Esox lucius (northern pike)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50538  
R;Mueller-Schmid, A.; Ganss, B.; Gorr, T.; Hoffmann, W.  
J. Mol. Evol. 36, 578-585, 1993  
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Clu  
A;Reference number: I50490; MUID:93353529; PMID:8350351  
A;Accession: I50538  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-221 <MUE>  
A;Cross-references: UNIPROT:P32188; UNIPARC:UPI000012A09D; GB:L09066; NID:g305096; PIDN:  
C;Genetics:  
A;Gene: Epd  
C;Superfamily: ependymin  
C;Keywords: Glycoprotein  
F;37,77,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 172.5; DB 2; Length 221;  
Best Local Similarity 25.8%; Pred. No. 2.4e-09;  
Matches 49; Conservative 34; Mismatches 94; Indels 13; Gaps 4;

Qy 2 PRCPQAPQWEGRWVYQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLY 61  
Db 30 PQHCTSPNMTGVLTVMALNGEIKATGHYHYDITDKKLRTFESDMHLKSEHLEDYLMLF 89

Qy 62 KDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGG---PQEQITVQEW---- 114  
Db 90 EGVFYDIDMKNQSKCKWLSHAHALELPAGAHQVELFLGSDTVQEEIKNIWTSV 149

Qy 115 SORKSARSYETWIGIYTKQCYVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTCQ 174  
Db 150 PETKGQYSVST-----TVGDCLPL-STFYSTDSTITLFSNSQVTEVKEPVFLSPSFCE 203

Qy 175 MAQLEKMS 184  
Db 204 GLELEDTHND 213

RESULT 4  
151377  
ependymin precursor - common carp  
C;Species: Cyprinus carpio (common carp)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I51377  
R;Adams, D.S.; Shashoua, V.E.  
Gene 141, 237-241, 1994  
A;Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.  
A;Reference number: I51377; MUID:94215910; PMID:8163195  
A;Accession: I51377  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-215 <ADA>  
A;Cross-references: UNIPROT:P38528; UNIPARC:UPI000012A09B; EMBL:U00432; NID:g397655; P  
C;Genetics:  
A;Gene: epn  
A;Introns: 28/1; 39/3; 84/3; 147/1; 175/2  
C;Superfamily: ependymin

Query Match 16.2%; Score 163; DB 2; Length 215;  
Best Local Similarity 24.2%; Pred. No. 2e-08;  
Matches 47; Conservative 45; Mismatches 84; Indels 18; Gaps 7;

Qy 3 RPOCAPQWEGRWVYQSSGRNSRAL--LSYDGLNQVRVLDERKALIPCKRLFEYILL 60  
Db 25 QPCHSPPLTSG--TMKVVSTGCHDLASGEFSYDSKANKRFVEDTAHANKTSHM-DVLVH 81

Qy 61 YKGVNMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGP---QEQITVQWSDR 117  
Db 82 FEEGVLYEDSKNESCKKETLQFRKHLMEIPPOATHESEIYMGSPSITEQGLRVRVNWK 141

Qy 118 ----KSARSYETWIGIYTKQCYVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTC 173  
Db 142 LPELHAHYSLST-----TSCGLPVSQSYGDKKDLIFS-FFGVETEVDQVFPVPAYC 195

Qy 174 QMAQLEKMS 187  
Db 196 EAVAFEEAPDDHSF 209

RESULT 5  
150490  
ependymin - Atlantic herring  
C;Species: Clupea harengus, Clupea harengus harengus (Atlantic herring)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50490  
R;Mueller-Schmid, A.; Ganss, B.; Gorr, T.; Hoffmann, W.  
J. Mol. Evol. 36, 578-585, 1993  
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Cl  
A;Reference number: I50490; MUID:93353529; PMID:8350351  
A;Accession: I50490  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-212 <MUE>  
A;Cross-references: UNIPROT:P32187; UNIPARC:UPI000012A09A; GB:L09065; NID:g304576; PIDN:  
C;Genetics:  
A;Gene: Epd  
C;Superfamily: ependymin  
C;Keywords: Glycoprotein  
F;69,92,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 162; DB 2; Length 212;  
Best Local Similarity 23.7%; Pred. No. 2.5e-08;





Query Match 14.7%; Score 148; DB 2; Length 216;  
Best Local Similarity 23.7%; Pred. NO. 5.9e-07;  
Matches 45; Conservative 43; Mismatches 92; Indels 10; Gaps 6;  
QY 3 RPOCAPOQWEGRWVYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFYILL 60  
DB 26 QPCHSPPLISG--TMKWVSTGGHDLASGEFSYDKANKRFRVSDAAHANKTSHT-DVLVH 82  
QY 61 YKGVNFQIDQATKQCSKMTLTQPDWPLDIPQNSTFEDQVSIQGP--OEOITVQWSDR 117  
DB 83 FEETUYEIDGKNESCKETLQFRKILMEIPDPATHESEIYMGSPSITTEGLAVRVWSGK 142  
QY 118 KSARSYETWIGIYTVKDCVPVQBTFTINYSVILSTRFFDIQLGKDPSPVFTPPSTCOMAQ 177  
DB 143 LPELHAHYSLSI-TSCGCLPVSGSYGDKDLLFS-FPGVETEDVDLQVFPVPAYCEGVA 200  
QY 178 LEKMSDECSW 187  
DB 201 FEEAPDDHSF 210  
RESULT 9  
E59435  
myosin IXA [imported] - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 09-Jul-2004  
R;Accession: E59435  
R;Gorman, S.W.; Haider, N.B.; Grieshammer, U.; Swiderski, R.E.; Kim, E.; Welch, J.W.; Se  
Genomics 59, 150-160, 1999  
A;Title: The cloning and developmental expression of unconventional myosin IXA (MYO9A) a  
A;Reference number: E59435  
A;Accession: E59435  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-2548 <GOR>  
A;Cross-references: UNIPROT:Q9UNJ2; UNIPARC:UPI000007206F; GB:NP\_008932; PID:G5902012; P  
Query Match 7.9%; Score 79.5; DB 2; Length 2548;  
Best Local Similarity 20.2%; Pred. No. 59;  
Matches 39; Conservative 26; Mismatches 77; Indels 51; Gaps 7;  
QY 4 PCQAPQWEGRWVYQSSGRNSRALI-----SYDGLNQRVRLDERKALIPCKRL 54  
DB 82 PVQOMLWP-RMALENRLSGEDYRFLRLKNDGSIHYGSLQSLRWLRVTEERRRM--ERG 138  
QY 55 FEYLLYKGVMFQIDQATKQCSKMTLTQPDWPLDIPQNSTFEDQVSIQGPQSIQVQEW 114  
DB 139 F-----LPQFQKDFDCLSLPDLNKTLLNL 166  
QY 115 SDRKSARSYETWIGI-YTVKDCVPVQBTFTINYSVILSTRFFD-IQLGKDPSPVFTPPST 172  
DB 167 RDRPKHEKIYTVGSILVINPFKFLIYNPKY-----VRMYDNHQLGKPEPHIYADV 221  
QY 173 COMAQLEKMSDC 185  
DB 222 AYHAMLQKKNQC 234  
RESULT 10  
C97109  
specialized DNA-dependent RNA polymerase sigma chain [imported] - Clostridium acetobutyli  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
R;Accession: C97109  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: C97109  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-257 <KUR>

A;Cross-references: UNIPROT:P33658; UNIPARC:UPI0000134848; GB:AE001437; PIDN:AAK79662.1  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC1696  
C;Superfamily: transcription sigma factor G; transcription initiation factor sigma katF  
Query Match 7.9%; Score 79; DB 2; Length 257;  
Best Local Similarity 22.5%; Pred. No. 4;  
Matches 39; Conservative 38; Mismatches 66; Indels 30; Gaps 8;  
QY 12 EGRQVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFEYLLYKGVNFQI 69  
DB 101 EIRRYLRDNNIRVSRSLRDIAVRLQVDRLLSKNNKEPTVSOIAKELKIPREVIKAL 160  
QY 70 DOATKQCSKMTLTQPDWPLDIPQNSTFEDQVSIQGPQSIQVQEWSDRKARSYETWIGI 129  
DB 161 DAIQ-----DPI-----SLFEPIYHDDGDAIVV-MDQISDNKNDL--DSWLQN 200  
QY 130 YTVKDCVPVQBTFTINYSVILSTRFFD--IQLGKDPSPVFTPPSTCOMAQLEK 180  
DB 201 ISIKE---AMKKLSREKMLNMRFFDGRQTQMEVADEIGI---SQAQVSRLEK 247  
RESULT 11  
I40621  
probable transcription initiation factor sigma G - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
R;Accession: I40621; I40628; S34310  
R;Sauer, U.; Treuner, A.; Buchholz, M.; Santangelo, J.D.; Durre, P.  
J. Bacteriol. 176, 6572-6582, 1994  
A;Title: Sporulation and primary sigma factor homologous genes in Clostridium acetobuty  
A;Reference number: I40609; MUID:95050216; PMID:7961408  
A;Accession: I40621  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-257 <RES>  
A;Cross-references: UNIPROT:P33658; UNIPARC:UPI0000134848; EMBL:Z23079; NID:G2437821; P  
R;Wong, J.; Sass, C.; Bennett, G.N.  
Gene 153, 89-92, 1995  
A;Title: Sequence and arrangement of genes encoding sigma factors in Clostridium acetob  
A;Reference number: I40626; MUID:95189110; PMID:7883192  
A;Accession: I40628  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-257 <RE2>  
A;Cross-references: UNIPARC:UPI000134848; EMBL:U07420; NID:G705344; PIDN:AAC43310.1; P  
R;Sauer, U.; Treuner, A.; Buchholz, M.; Duerre, P.  
submitted to the EMBL Data Library, June 1993  
A;Description: Sigma factor homologous genes in C. acetobutylicum.  
A;Reference number: S34306  
A;Accession: S34310  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 24-145, 'G', 147, 'G', 150, 'NTSPRSD', 158-257 <SAU>  
A;Cross-references: UNIPARC:UPI000017576F; EMBL:Z23079  
C;Genetics:  
A;Gene: sigG  
A;Start codon: GTG  
C;Superfamily: transcription sigma factor G; transcription initiation factor sigma katF  
C;Keywords: DNA binding; sigma factor; transcription initiation  
F;44-257/Domain: transcription initiation factor sigma katF homology <KTF>  
Query Match 7.9%; Score 79; DB 2; Length 257;  
Best Local Similarity 22.5%; Pred. No. 4;  
Matches 39; Conservative 38; Mismatches 66; Indels 30; Gaps 8;  
QY 12 EGRQVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFEYLLYKGVNFQI 69  
DB 101 EIRRYLRDNNIRVSRSLRDIAVRLQVDRLLSKNNKEPTVSOIAKELKIPREVIKAL 160  
QY 70 DOATKQCSKMTLTQPDWPLDIPQNSTFEDQVSIQGPQSIQVQEWSDRKARSYETWIGI 129  
DB 161 DAIQ-----DPI-----SLFEPIYHDDGDAIVV-MDQISDNKNDL--DSWLQN 200



Db 161 DAIQ-----DPI-----SLFPIYHDDGDAIYV-MDQISDNKULD--DSWLQN 200  
QY 130 YTVKDCYVQVETFTINYSVILSTRFFD--IQLGIKDPVSFTPPSTCQMAQLEK 180  
Db 201 ISIKE---AMKLSDRKXWILNMRFFDGRTOQEVADEIGI---SQAQVSRLK 247

## RESULT 12

A72319 conserved hypothetical protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: A72319  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: A72319  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-275 <ARN>  
A:Cross-references: UNIPROT:Q9X008; UNIPARC:UPI00000C135F; GB:AE001755; GB:AE000512; NID  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0906  
C:Superfamily: Bacillus subtilis flagellar probable biosynthesis switch protein ylxH

Query Match 7.8%; Score 78.5; DB 2; Length 275;  
Best Local Similarity 25.2%; Pred. No. 4.9;  
Matches 37; Conservative 26; Mismatches 65; Indels 19; Gaps 7;  
QY 21 SSGRNSRALLSYDGLNORVRLDERKALIPCKRLFEVILL-YKQGVMFQIDQATKQCSKM 79  
Db 94 SSGIDMEDLIUN-LGDRRRFFEFARLL-----RKDYLVLDVPPGYNENLDFYIQSDFL 149  
QY 80 TLTPQWPLDIPQNSTFEDQYSIGG--PQEQITVQEW-----SDRSARSYETWI 127  
Db 150 ILVTSPEPTSIINTYLIKLSVKGITPEEFILVNMVNMKEGRLAADRLK-RVVERFV 208  
QY 128 GIYTVKDCYVQVETFTINYSVILSTRF 154  
Db 209 G-FTIKNYFIKEDQVQVRSVFLQEPF 234

## RESULT 13

I55184 repA protein - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
C:Accession: I55184; S34178  
R:Llanes, C.; Gabant, P.; Couturier, M.; Michel-Briand, Y.  
J. Bacteriol. 76, 3403-3407, 1993  
A:Title: Cloning and characterization of the Inc A/C plasmid RAL replicon.  
A:Reference number: I55184  
A:Accession: I55184  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-288 <RES>  
A:Cross-references: UNIPROT:Q08896; UNIPARC:UPI00000B9B5C; EMBL:X73674; NID:g313284; PID  
C:Genetics:  
A:Gene: repA

Query Match 7.8%; Score 78; DB 2; Length 288;  
Best Local Similarity 24.0%; Pred. No. 5.8;  
Matches 37; Conservative 34; Mismatches 49; Indels 34; Gaps 8;  
QY 25 NSRALLSYDGLNORVRLDE--RKALIPCKRLFEVILLYKQGVMFQIDQATKQCSKM--- 79  
Db 102 DGRTVLIYAG--QREELIEDALRKLAVNGK---GHIEGKAGVMTFLYELQKLSKMGHG 156  
QY 80 -TLTPQWPLDIPQNSTFEDQYSIGGPGQEQITVQEWSDRSARSYETWIGIYTVKD---- 134

Db 157 YNLTEIKAIQVCRGATLE-----CISDDGEAFISSFFPMVGLTTRGEFRKK 204  
QY 135 -----CYPVQVETFTINYSVI-LSTRFFDIQLGIK 162  
Db 205 GGNARCY-VQPNPLVNESIMNLSFRQYNYKIGMQ 237

## RESULT 14

E70834 probable regulatory protein with some - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: E70834  
R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,  
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,  
Rajandream, M.A.; Rogers, R.; Sulston, J.; Rutter, S.; Seger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: E70834  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1085 <COL>  
A:Cross-references: UNIPROT:O53720; UNIPARC:UPI000016521A; GB:AL021931; GB:AL123456; N  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV0386

Query Match 7.8%; Score 78; DB 2; Length 1085;  
Best Local Similarity 22.9%; Pred. No. 29;  
Matches 50; Conservative 34; Mismatches 68; Indels 66; Gaps 12;  
QY 5 COAPQOQWEGROVMYQ-QSSGRNSRALLSYDGLNORV-----RVLDERKALIP--CKRLFEY 57  
Db 324 CREPLRVEG-EVSVRVPSSLSDAEMFCYRAQVRPDRFLTDDNSAAVTEICKRL---- 379  
QY 58 ILLYKQGVMFQIDQATKQCKMTLTQPDWPLDIPQNSTFEDQYSI--GGPQEQITVQ--- 112  
Db 380 -----DGLPLAIELAARLSMTLDEIDGL-----RDRFALLTGARTAAHRQQT 426  
QY 113 -----EWS-----DRKSARSYETWIGIYTVKDCVPV-----OBTFTINYSV 148  
Db 427 WASVDWSYTLTTEPERTLFRRLAVFVGCFVDDAQAVACSGDVQRYQVLDLITLLVDSKL 486  
QY 149 ILSTRFFDIQLGIKDPVSFTPPSTCQMAQ---LERMSE 183  
Db 487 VMA-----DDNSGRTCYRLCETMRHYALEKLSE 514

## RESULT 15

S46686 hypothetical protein YHR186c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein H9998.14  
C:Species: Saccharomyces cerevisiae  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: S46686  
R:Macri, C.  
submitted to the EMBL Data Library, February 1994  
A:Description: The sequence of S. cerevisiae cosmid 9998.  
A:Reference number: S46674  
A:Accession: S46686  
A:Molecule type: DNA  
A:Residues: 1-1541 <MAC>  
A:Cross-references: UNIPROT:P38873; UNIPARC:UPI000013B2F6; EMBL:U00030; NID:g458927; P  
C:Genetics:  
A:Cross-references: SGD:S0001229  
A:Map position: 8R  
C:Keywords: transmembrane protein

Query Match 7.8%; Score 78; DB 2; Length 1541;  
Best Local Similarity 20.7%; Pred. No. 45;

Matches	41;	Conservative	27;	Mismatches	74;	Indels	56;	Gaps	10;
Qy	4	PCQAPQOWEGRQVWYQSS-----GRNSRALLSYDGLNORVRLDERKALIPCKRLFEY	57						
Db	89	PCARVEAWVD-PLNFQDSKKAIEQIGNLQA--QYETLSLRTRY---KQSLDFC-----	136						
Qy	58	ILLYKDGVMFQIDQATKQCCKMTLTQFWDPLDIPQNSTFEDQYSIGGPQEQITVQEWSDR	117						
Db	137	-----VEDVKRFCSNLSARTSKEDRILFHYNH-----GVPKPTKSGEIWFN	178						
Qy	118	KSARSY-----ETWIG--IYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPVSF	167						
Db	179	RGYTQIPVSLYDLQTLGAPCIFYVDCNSA-ENILINFOKFVQKRIKDDDEGNHDAAP	237						
Qy	168	TPPSTCQMAQLKMSDC	185						
Db	238	SPTSAYQ-----DC	246						

Search completed: June 10, 2006, 03:11:20  
Job time : 43 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:02:19 ; Search time 296 seconds  
(without alignment)  
584.385 Million cell updates/sec

Title: US-10-733-646-2\_COPY\_38\_224

Perfect score: 1005

Sequence: 1 APRFCAPQAGWGRVYQQ.....TPPSTCQMAQLKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	100.0	224	1	EPDRI_HUMAN
2	997	99.2	344	2	Q96J80_homo sapien
3	991	98.5	224	2	Q99M77_mus musculus
4	978	97.3	227	2	Q95K54_MACFA
5	974	96.9	227	1	EPDRI_MACFA
6	974	96.9	227	2	Q95K77_MACFA
7	941	93.6	218	2	Q95K56_macaca fasc
8	886	88.2	224	2	Q5X110_RAT
9	875	87.1	224	2	Q99M71_m mammalian
10	869	86.5	224	2	Q8CA12_MOUSE
11	861	85.7	224	2	Q8BQV1_MOUSE
12	671	66.8	206	2	Q6DH25_BRARE
13	434.5	43.2	234	2	Q6EEF4_9ECHN
14	288	28.7	194	2	Q61WN5_BRABE
15	186	18.5	211	2	Q4TFW4_TETNG
16	181	18.0	181	2	Q90394_STELE
17	180.5	18.0	221	1	EPD2_ONCMY
18	177.5	17.7	221	1	EPD2_SALSA
19	177	17.6	178	2	Q91083_9TELE
20	174.5	17.4	175	2	Q91140_9TELE
21	173.5	17.3	221	1	EPD1_ONCMY
22	173	17.2	178	2	Q91253_9TELE
23	173	17.2	221	1	EPD109_9TELE
24	172.5	17.2	221	1	EPD_ESOLU
25	172	17.1	178	2	Q91052_9TELE
26	164.5	16.4	183	2	Q90492_9TELE
27	163	16.2	215	1	EPD_CYBCA
28	162	16.1	212	1	EPD_CLUNA
29	158	15.7	218	1	EPD_DANAE
30	155.5	15.5	216	2	Q4S8U8_TETNG
31	154	15.3	180	2	Q91331_9TELE

32	153.5	15.3	214	1	EPD_NOTCH	Q91130 notropis ch
33	152.5	15.2	186	2	Q91465_9TELE	Q91465 synodontis
34	152	15.1	215	1	EPD1_CARAU	P13506 carassius a
35	151	15.0	217	1	EPD_BRARE	P17561 brachydanio
36	148	14.7	170	2	Q90241_9TELE	Q90241 alestes sp.
37	148	14.7	215	1	EPD2_CARAU	P12958 carassius a
38	147.5	14.7	136	2	Q91254_9TELE	Q91254 paracheiroid
39	146	14.5	172	2	Q91057_9TELE	Q91057 hemiodus sp
40	132.5	13.2	140	2	Q91045_9TELE	Q91045 gastetopele
41	131	13.0	203	2	Q6WNG6_BRABE	Q6WNG6 branchioero
42	129.5	12.9	131	2	Q90276_9TELE	Q90276 boulergerel
43	125.5	12.5	137	2	Q91058_9TELE	Q91058 hoplias sp.
44	125	12.4	192	2	Q91464_9TELE	Q91464 schilbe sp.
45	123	12.2	133	2	Q91059_9TELE	Q91059 hypostomus

#### ALIGNMENTS

RESULT 1  
EPDRI\_HUMAN  
ID EPDRI\_HUMAN STANDARD; PRT; 224 AA.  
AC Q9UM22;  
21-FEB-2001, integrated into UniProtKB/Swiss-Prot.  
DT 21-FEB-2001, sequence version 2.  
DT 07-FEB-2006, entry version 40.  
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).  
DE protein).  
GN Name=EPDRI; Synonyms=MERP1, UCC1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M., Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.; "Identification and characterization of a novel family of mammalian ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic, RT and malignant tissues.";  
RL DNA Cell Biol. 20:625-635(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Cervix;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blackley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 51-224.  
RA Nimrich I., Erdmann S., Melchers U.; "Genes that are differentially expressed in colon cancer.";  
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Secreted protein.

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CC -I- SIMILARITY: Belongs to the ependymin family.
CC -----
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CC -----
DR EMBL; AF361252; AAK26441.1; -; Genomic DNA.
DR EMBL; BC006866; AAK00686.2; ALT INIT; mRNA.
DR EMBL; BC018299; AAK18299.1; -; mRNA.
DR EMBL; AJ250475; CAB60269.1; ALT INIT; mRNA.
DR Ensembl; ENSG00000086289; Homo sapiens.
DR HGNC; HGNC:17572; EPDR1.
DR LinkHub; Q9UM22; -.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; 1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 37 Potential.
FT CHAIN 38 224 Mammalian ependymin-related protein 1.
FT /FTID=PRO_0000008351.
FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CONFLICT 207 207 P -> S (in Ref. 3).
SQ SEQUENCE 224 AA; 25437 MW; 84ADBA3666261611 CRC64;

Query Match 100.0%; Score 1005; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. NO. 1.6e-91; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0;

QY 1 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 60
DB 38 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 97
QY 61 YKGVNFQIDQATKQCKMTLTQWPDLIPQNSTFEDQYISGPOEQITVQWSDRKS 120
DB 98 YKGVNFQIDQATKQCKMTLTQWPDLIPQNSTFEDQYISGPOEQITVQWSDRKS 157
QY 121 RSYETWIGIYTVKDCVPQVETFTINYSVILSTRFFDIQLGKDPSPVTPSTCMAQLEK 180
DB 158 RSYETWIGIYTVKDCVPQVETFTINYSVILSTRFFDIQLGKDPSPVTPSTCMAQLEK 217
QY 181 MSDDCSW 187
DB 218 MSDDCSW 224

RESULT 2
Q96J80 HUMAN PRELIMINARY; PRT; 344 AA.
AC Q96J80;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Mammalian ependymin related protein 1.
GN Name=EPDR1; Synonyms=MERP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues."
RL DNA Cell Biol. 20:625-635(2001).
CC [2]
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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21940632; PubMed=11943480; DOI=10.1016/S0378-1119(02)00434-1;
RA Gregorio-King C.C., McLeod J.L., Collier F.M., Collier G.R.,
RA Bolton K.A., Van Der Meer G.J., Apostolopoulos J., Kirkland M.A.;
RT "MERP1: a mammalian ependymin-related protein gene differentially
RT expressed in hematopoietic cells."
RL Gene 286:249-257(2002).
CC -----
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CC -----
DR EMBL; AY027862; AAK15788.2; -; mRNA.
DR Ensembl; ENSG00000086289; Homo sapiens.
DR HGNC; HGNC:17572; EPDR1.
DR LinkHub; Q96J80; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN 1.
SQ SEQUENCE 344 AA; 38141 MW; 34D75B84822692DA CRC64;

Query Match 99.2%; Score 997; DB 2; Length 344;
Best Local Similarity 99.5%; Pred. NO. 1.7e-90;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 60
DB 158 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 217
QY 61 YKGVNFQIDQATKQCKMTLTQWPDLIPQNSTFEDQYISGPOEQITVQWSDRKS 120
DB 218 YKGVNFQIDQATKQCKMTLTQWPDLIPQNSTFEDQYISGPOEQITVQWSDRKS 277
QY 121 RSYETWIGIYTVKDCVPQVETFTINYSVILSTRFFDIQLGKDPSPVTPSTCMAQLEK 180
DB 278 RSYETWIGIYTVKDCVPQVETFTINYSVILSTRFFDIQLGKDPSPVTPSTCMAQLEK 337
QY 181 MSDDCSW 187
DB 338 MSDDCSW 344

RESULT 3
Q99M77 MOUSE PRELIMINARY; PRT; 224 AA.
AC Q99M77;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Mammalian ependymin related protein 1.
GN Name=Ucci; Synonyms=Epdr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues."
RL DNA Cell Biol. 20:625-635(2001).
CC -----
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EMBL; AY027861; AAK15787.1; -, mRNA.  
MGI; MGI:2152290; Epdrl.  
MGI; MGI:2152290; Ucc1.  
GO; GO:0005576; C:extracellular region; IEA.  
GO; GO:0005509; F:calcium ion binding; IEA.  
GO; GO:0007160; P:cell-matrix adhesion; IEA.  
InterPro; IPR001299; Ependymin.  
PANTHER; PTHR10697; Ependymin, 1.  
PRINTS; PR00317; EPENDYMIN.  
ProDom; PD006315; Ependymin, 1.  
PROSITE; PS00898; Ependymin\_1; UNKNOWN\_1.  
PROSITE; PS00899; EPENDYMIN\_2; 1.  
SEQUENCE 224 AA; 25437 MW; DB6A5A9A7289E95 CRC64;

Query Match 98.6%; Score 991; DB 2; Length 224;  
Best Local Similarity 99.5%; Pred. No. 3.9e-90;  
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFYILL 60  
Db 38 APRPCAPQWEGQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFYILL 97

QY 61 YKGVMFQIDQATKQCKSMILTQPDPLDPONSTFEDQYSGPQEQITVQWSDRKS 120  
Db 98 YKGVMFQIDQATKQCKSMILTQPDPLDPONSTFEDQYSGPQEQITVQWSDRKS 157

QY 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTPSTCMAOLEK 180  
Db 158 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTPSTCMAOLEK 217

QY 181 MSEDCSW 187  
Db 218 MSEDCSW 224

RESULT 4  
Q95K54 MACFA  
ID Q95K54\_MACFA PRELIMINARY; PRT; 227 AA.  
AC Q95K54;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 15.  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Medulla oblongata;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
libraries";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
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EMBL; AB066337; BAB62213.1; -, mRNA.  
GO; GO:0005576; C:extracellular region; IEA.  
GO; GO:0005509; F:calcium ion binding; IEA.  
GO; GO:0007160; P:cell-matrix adhesion; IEA.  
InterPro; IPR001299; Ependymin.  
PANTHER; PTHR10697; Ependymin, 1.  
PRINTS; PR00317; EPENDYMIN.  
ProDom; PD006315; Ependymin, 1.  
PROSITE; PS00898; Ependymin\_1; UNKNOWN\_1.  
PROSITE; PS00899; EPENDYMIN\_2; 1.  
Hypothetical protein.

SQ SEQUENCE 227 AA; 25850 MW; 3963EAB6D5F016F4 CRC64;

Query Match 97.3%; Score 978; DB 2; Length 227;  
Best Local Similarity 96.8%; Pred. No. 7.8e-89;  
Matches 181; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFYILL 60  
Db 41 APRPCAPQWEGQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFYILL 100

QY 61 YKGVMFQIDQATKQCKSMILTQPDPLDPONSTFEDQYSGPQEQITVQWSDRKS 120  
Db 101 YKGVMFQIDQATKQCKSMILTQPDPLDPONSTFEDQYSGPQEQITVQWSDRKS 160

QY 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTPSTCMAOLEK 180  
Db 161 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTPSTCMAOLEK 220

QY 181 MSEDCSW 187  
Db 221 MSEDCSW 227

RESULT 5  
EPDRL MACFA  
ID EPDRL MACFA STANDARD; PRT; 224 AA.  
AC Q9NOC7;  
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.  
DT 21-FEB-2001, sequence version 2.  
DT 07-FEB-2006, entry version 31.  
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).  
GN Name=EPDRL; Synonyms=MERP1, UCC1; ORFNames=QcCE-12983;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC Tissue=Brain cortex;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
libraries";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Secreted protein.  
CC -!- SIMILARITY: Belongs to the ependymin family.  
CC -----  
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EMBL; AB046003; BAB01585.1; ALT\_INIT; mRNA.  
LinkHub; Q9NOC7; -  
InterPro; IPR001299; Ependymin.  
PANTHER; PTHR10697; Ependymin, 1.  
PRINTS; PR00317; EPENDYMIN.  
ProDom; PD006315; Ependymin, 1.  
PROSITE; PS00898; Ependymin\_1; 1.  
PROSITE; PS00899; EPENDYMIN\_2; 1.  
KW Glycoprotein; signal.  
FT SIGNAL 1 37 Potential.  
FT CHAIN 38 224 Mammalian ependymin-related protein 1.  
FT /FTID=PRO\_0000008352.  
FT CARBOHYD 130 130 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 182 182 N-linked (GlcNAc...) (potential).  
SQ SEQUENCE 224 AA; 25484 MW; 3594311D15AB4B7 CRC64;

Query Match 96.9%; Score 974; DB 1; Length 224;  
Best Local Similarity 96.8%; Pred. No. 1.9e-88;  
Matches 181; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFYILL 60

Qy	1	APRPCAPQWEGROVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILL	60
Db	41	APRPCAPQWEGROVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILL	100
Qy	61	YKGVNMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQITVOEWSDRKSA	120
Db	101	YKGVNMFQIEQATKQCSKMTLTPEWPDPLDIPQNSTFEDQYSIGGPOEQIMVQEWSDRKSA	160
Qy	121	RSYETWIGIYTVKDCYPVOETFTINYSVILSTRFRFDIQLGDKDPSVFTPPSTCQMAQLEK	180
Db	161	RSYETWIGIYTVKDCYPVOETFTKNYSVILSTRFRFDIQLGDKDPSVFTPPSTCQIAQLEK	220
Qy	181	MSDCSW 187	
Db	221	MSDCSW 227	
RESULT 7			
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AC	Q95K56		
DT	01-DEC-2001,	integrated into UniProtKB/TrEMBL.	
DT	01-DEC-2001,	sequence version 1.	
DT	07-FEB-2006,	entry version 15.	
DE	Hypothetical protein.		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
OC	Cercopitheidae; Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9541;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Medulla oblongata;		
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,		
RA	Suzuki Y., Sugano S., Hashimoto K.;		
RT	"Isolation of full-length cDNA clones from macaque brain cDNA		
RT	libraries.";		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
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CC	-----		
DR	EMBL;	AB065535; BAB62211.1; -; mRNA.	
DR	GO;	GO:0005576; C:extracellular region; IEA.	
DR	GO;	GO:0005509; F:calcium ion binding; IEA.	
DR	GO;	GO:0007160; P:cell-matrix adhesion; IEA.	
DR	InterPro;	IPR001299; Ependymin.	
DR	PANTHER;	PTHR10697; Ependymin; 1.	
DR	PRINTS;	PR00317; EPENDYMIN.	
DR	PRODOM;	PD006315; Ependymin; 1.	
DR	PROSITE;	PS00898; EPENDYMIN_1; UNKNOWN_1.	
DR	PROSITE;	PS00899; EPENDYMIN_2; 1.	
KW	Hypothetical protein.		
SQ	SEQUENCE 218 AA; 24970 MW; 8B8524C0D98677C CRC64;		
Query Match 93.6%; Score 941; DB 2; Length 218;			
Best Local Similarity 96.7%; Pred. No. 3.6e-85; Indels 0; Gaps 0;			
Matches 175; Conservative 4; Mismatches 2; Indels 0; Gaps 0;			
Qy	7	APQWEGROVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVM	66
Db	38	APQWEGROVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVM	97
Qy	67	FQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQITVOEWSDRKSARSYETW	126
Db	98	FQIEQATKQCSKMTLTPEWPDPLDIPQNSTFEDQYSIGGPOEQIMVQEWSDRKSARSYETW	157
Qy	127	IGIYTVKDCYPVOETFTINYSVILSTRFRFDIQLGDKDPSVFTPPSTCQMAQLEKSDCS	186
Db	158	IGIYTVKDCYPVOETFTKNYSVILSTRFRFDIQLGDKDPSVFTPPSTCQIAQLEKSDCS	217
Qy	187	W 187	

Db	38	APRPCAPQWEGROVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILL	97
Qy	61	YKGVNMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQITVOEWSDRKSA	120
Db	98	YKGVNMFQIEQATKQCSKMTLTPEWPDPLDIPQNSTFEDQYSIGGPOEQIMVQEWSDRKSA	157
Qy	121	RSYETWIGIYTVKDCYPVOETFTINYSVILSTRFRFDIQLGDKDPSVFTPPSTCQMAQLEK	180
Db	158	RSYETWIGIYTVKDCYPVOETFTKNYSVILSTRFRFDIQLGDKDPSVFTPPSTCQIAQLEK	217
Qy	181	MSDCSW 187	
Db	218	MSDCSW 224	
RESULT 6			
ID	Q95K77	MACFA PRELIMINARY; PRT; 227 AA.	
AC	Q95K77		
DT	01-DEC-2001,	integrated into UniProtKB/TrEMBL.	
DT	01-DEC-2001,	sequence version 1.	
DT	07-FEB-2006,	entry version 17.	
DE	Hypothetical protein.		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
OC	Cercopitheidae; Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9541;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Temporal lobe right;		
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,		
RA	Suzuki Y., Sugano S., Hashimoto K.;		
RT	"Isolation of full-length cDNA clones from macaque brain cDNA		
RT	libraries.";		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Medulla oblongata;		
RX	MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;		
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M.,		
RA	Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;		
RT	"Assignment of 118 novel cDNAs of cynomolgus monkey brain to human		
RT	chromosomes.";		
RL	Gene 275:31-37(2001).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Medulla oblongata;		
RA	Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;		
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.		
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CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC	-----		
DR	EMBL;	AB063094; BAB60800.1; -; mRNA.	
DR	ENBL;	AB097520; BAC41745.1; -; mRNA.	
DR	GO;	GO:0005576; C:extracellular region; IEA.	
DR	GO;	GO:0005509; F:calcium ion binding; IEA.	
DR	GO;	GO:0007160; P:cell-matrix adhesion; IEA.	
DR	InterPro;	IPR001299; Ependymin.	
DR	PANTHER;	PTHR10697; Ependymin; 1.	
DR	PRINTS;	PR00317; EPENDYMIN.	
DR	PRODOM;	PD006315; Ependymin; 1.	
DR	PROSITE;	PS00898; EPENDYMIN_1; UNKNOWN_1.	
DR	PROSITE;	PS00899; EPENDYMIN_2; 1.	
KW	Hypothetical protein.		
SQ	SEQUENCE 227 AA; 25821 MW; BE6A77C5867DA50A CRC64;		
Query Match 96.9%; Score 974; DB 2; Length 227;			
Best Local Similarity 96.8%; Pred. No. 2e-88; Indels 0; Gaps 0;			
Matches 181; Conservative 3; Mismatches 3; Indels 0; Gaps 0;			

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DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Ependymin related protein 2.
GN Name=Ependr2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RP Rattus norvegicus (Rat).
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Zeeberg B., Buotow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP Rattus norvegicus.
RC TISSUE=Heart;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC083701; AAH83701.1; -; mRNA.
DR Ensembl; ENSRNOG0000018989; Rattus norvegicus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10497; Ependymin; 1.
DR PRINTS; PD00317; EPENDYMN.
DR ProDom; PD006315; Ependymin; 1.
SQ SEQUENCE 224 AA; 25639 MW; B8DE78133B1CCB21 CRC64;
Query Match 88.2%; Score 886; DB 2; Length 224;
Best Local Similarity 86.5%; Pred. No. 1.1e-79;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;
Qy 2 PRPQAPQWEGROWVYQSSGRNRLSLVSDGLNQRVRLDERKALIPCKRLFEYILLY 61
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Qy 62 KGVNMFQIDQATKQCSKWTLPQWDPDLPQNSTFEDQYSIGGPQEQITVQWSDRSAR 121
Db 99 KGVNMFQIEQATKCAKTIPLAEPDPLDIPQNSTFEDQYSIGGPQEQIMVQWSDRSAR 158
Qy 122 SYETWIGYTVKDCYPVQVQETFTINYSVILSTRFFDIQIGKIDPSVFTTPTSCQMAQLEKM 181
Db 159 SYETWIGYTVKDCYPVQVQETFTINYSVILSTRFFDIQIGKIDPSVFTTPTSCQMAQLEKM 218
Qy 182 SEDCS 186
Db 219 KENCS 223
RESULT 9
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AC Q99W71;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Mammalian ependymin related protein-2 (Ependymin 2) (Adult male
DE diencephalon cDNA, RIKEN full-length enriched library,
DE clone:9330154003 product:mammalian ependymin related protein-2) (Adult
DE male cerebellum cDNA, RIKEN full-length enriched library,
DE clone:1500034M21 product:Mammalian ependymin related protein-2
DE (Similar to mammalian ependymin related protein 1), full insert
DE sequence).
GN Name=Epd2; Synonyms=AU040950, MERP2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP Mus musculus (Mouse).
RC MEDLINE=21622606; PubMed=11749721; DOI=10.1089/10454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues.";
RL DNA Cell Biol. 20:625-635 (2001).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schenken C.M., Schuler G.D.,
RA Alschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Kidney;
RC Director MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
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RT "high-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999). [5]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; PubMed=16141072; DOI=10.1126/science.1112014;

RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apeilner R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.B., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Petrowsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K., Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamashiro H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojiwa M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami T., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;

RA "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). [6]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; PubMed=16141073; DOI=10.1126/science.1112009;

RX RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;

RG "Antisense transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005). [7]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; MEDLINE=22354683; PubMed=10246685; DOI=10.1038/nature01266;

RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirokawa T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Shiraaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002). [8]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bono M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). [9]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RA "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). [10]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RA "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000). [11]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=diencephalon;

RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

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Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

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 16-AUG-2004, sequence version 1.  
 07-FEB-2006, entry version 8.  
 Ependymin-related protein precursor.  
 Name=Epen;  
 Holothuria glaberrima.  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Holothuriida; Aspidochirotea; Aspidochirotida; Holothuriidae;  
 Holothuria.  
 NCBI\_TaxID=311192;  
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 NUCLEOTIDE SEQUENCE.  
 PubMed15256263; DOI=10.1016/j.gene.2004.03.023;  
 Suarez-Castillo E.C., Medina-Ortiz W.E., Roig-Lopez J.L.,  
 Garcia-Araras J.E.;  
 "Ependymin, a gene involved in regeneration and neuroplasticity in  
 vertebrates, is overexpressed during regeneration in the echinoderm  
 Holothuria glaberrima.";  
 Gene 334:133-143(2004).  
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 EMBL; AY383544; AAR89380.1; -; mRNA.  
 GO; GO:0005576; C:extracellular region; IEA.  
 GO; GO:0005509; P:calcium ion binding; IEA.  
 GO; GO:0007160; P:cell-matrix adhesion; IEA.  
 InterPro; IPR001299; Ependymin.  
 PANTHER; PTHR10697; Ependymin; 1.  
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 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE Ependymin related protein-1.  
 OS Branchiostoma belcheri tsingtaunense.  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
 OC Branchiostoma.  
 NCBI\_TaxID=155462;  
 [1]  
 NUCLEOTIDE SEQUENCE.  
 Zhang S., Liu Z., Li H., Fan C., Li L., Xu A.;  
 Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
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 EMBL; AY616185; AAT39416.1; -; mRNA.  
 CC



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Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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Run on: June 10, 2006, 03:10:49 ; Search time 49 Seconds  
(without alignment)  
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Title: US-10-733-646-2\_COPY\_38\_224  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 650591 seqs, 87530628 residues  
Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Issued Patents AA:\*  
1: /EMC Celerra\_SID33/ptodata/2/iaa/5 COMB.pep:\*  
2: /EMC Celerra\_SID33/ptodata/2/iaa/6 COMB.pep:\*  
3: /EMC Celerra\_SID33/ptodata/2/iaa/7 COMB.pep:\*  
4: /EMC Celerra\_SID33/ptodata/2/iaa/H COMB.pep:\*  
5: /EMC Celerra\_SID33/ptodata/2/iaa/PCTUS COMB.pep:\*  
6: /EMC Celerra\_SID33/ptodata/2/iaa/RE COMB.pep:\*  
7: /EMC Celerra\_SID33/ptodata/2/iaa/backfiles1.pep:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1005	100.0	187 2	US-09-242-890-1 Sequence 1, Appli
2	1005	100.0	200 2	US-09-242-890-10 Sequence 10, Appli
3	1005	100.0	224 2	US-09-229-583A-2 Sequence 2, Appli
4	1005	100.0	224 2	US-09-242-890-11 Sequence 11, Appli
5	1005	100.0	224 2	US-10-187-904-2 Sequence 2, Appli
6	886	88.2	190 2	US-09-242-890-2 Sequence 2, Appli
7	886	88.2	224 2	US-09-242-890-12 Sequence 12, Appli
8	875	87.1	187 2	US-09-242-890-3 Sequence 3, Appli
9	875	87.1	224 2	US-09-242-890-13 Sequence 13, Appli
10	201	20.0	39 2	US-09-242-890-8 Sequence 8, Appli
11	180.5	18.0	221 2	US-09-229-583A-4 Sequence 4, Appli
12	180.5	18.0	221 2	US-10-187-904-4 Sequence 4, Appli
13	175	17.4	32 2	US-09-242-890-5 Sequence 5, Appli
14	163	16.2	215 2	US-09-229-583A-5 Sequence 5, Appli
15	163	16.2	215 2	US-10-187-904-5 Sequence 5, Appli
16	162	16.1	212 2	US-09-229-583A-7 Sequence 7, Appli
17	162	16.1	212 2	US-10-187-904-7 Sequence 7, Appli
18	151	15.0	217 2	US-09-229-583A-6 Sequence 6, Appli
19	151	15.0	217 2	US-10-187-904-6 Sequence 6, Appli
20	148	14.7	216 2	US-09-229-583A-3 Sequence 3, Appli
21	148	14.7	216 2	US-10-187-904-3 Sequence 3, Appli
22	147	14.6	26 2	US-09-242-890-9 Sequence 9, Appli
23	143	14.2	25 2	US-09-242-890-6 Sequence 6, Appli
24	93	9.3	17 2	US-09-242-890-7 Sequence 7, Appli
25	82	8.2	419 2	US-09-134-001C-4658 Sequence 4658, Ap
26	79.5	7.9	2548 2	US-09-172-422-1 Sequence 1, Appli

27	78	7.8	13	2	US-09-242-890-4	Sequence 4, Appli
28	77	7.7	617	2	US-09-614-912-138	Sequence 138, App
29	76	7.6	1296	2	US-09-614-912-140	Sequence 140, App
30	74.5	7.4	615	2	US-08-676-444-44	Sequence 44, Appli
31	74	7.4	263	2	US-09-248-796A-15254	Sequence 15254, A
32	73.5	7.3	710	2	US-09-489-039A-14121	Sequence 14121, A
33	73	7.3	388	2	US-09-489-039A-11478	Sequence 11478, A
34	73	7.3	483	2	US-10-104-047-3911	Sequence 3911, Ap
35	73	7.3	749	2	US-09-328-352-7588	Sequence 7588, Ap
36	71.5	7.1	399	2	US-09-248-796A-18089	Sequence 18089, A
37	70	7.0	227	2	US-09-710-279-2396	Sequence 2396, Ap
38	69	6.9	2291	2	US-09-822-871-2	Sequence 2, Appli
39	68.5	6.8	215	2	US-09-107-433-4726	Sequence 4726, Ap
40	68.5	6.8	371	2	US-09-538-092-630	Sequence 630, App
41	68.5	6.8	481	2	US-09-489-039A-7805	Sequence 7805, App
42	68.5	6.8	495	2	US-10-094-749-2349	Sequence 2349, Ap
43	68	6.8	521	1	US-08-659-251-3	Sequence 3, Appli
44	68	6.8	521	2	US-09-256-490-3	Sequence 3, Appli
45	68	6.8	521	5	PCT-US96-11445-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-242-890-1  
; Sequence 1, Application US/09242890.  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; APPLICANT: Onda, Haruo  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 241TUSOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 1  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Human  
US-09-242-890-1

Query Match					100.0%;	Score 1005;	DB 2;	Length 187;
Best Local Similarity					100.0%;	Pred. No. 8.7e-11;	Indels 0;	Gaps 0;
Matches 187;					Conservative 0;	Mismatches 0;		
Qy	1	APRPCAPQWEGRVYQQSSGRNSRALLSYDGLNORVRLDERKALIPCKRLFEYILL	60					
Db	1	APRPCAPQWEGRVYQQSSGRNSRALLSYDGLNORVRLDERKALIPCKRLFEYILL	60					
Qy	61	YKDGVMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVOEWSDRKSA	120					
Db	61	YKDGVMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVOEWSDRKSA	120					
Qy	121	RSVETWIGITVKDCYPQVETFTINYSVILSTRFDIQLGKDPSTVTPPTCQMAQLEK	180					
Db	121	RSVETWIGITVKDCYPQVETFTINYSVILSTRFDIQLGKDPSTVTPPTCQMAQLEK	180					
Qy	181	MSEDCSW	187					
Db	181	MSEDCSW	187					
RESULT 2								

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US-09-242-890-10
; Sequence 10, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Human
; US-09-242-890-10

Query Match      100.0%; Score 1005; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 9.6e-111;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFVILL 60
Db 14 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFVILL 73
QY 61 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYISGGPQEQITVQSWDRKSA 120
Db 74 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYISGGPQEQITVQSWDRKSA 133
QY 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAQLEK 180
Db 134 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAQLEK 193
QY 181 MSEDSCSW 187
Db 194 MSEDSCSW 200

RESULT 3
US-09-229-583A-2
; Sequence 2, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-229-583A-2

Query Match      100.0%; Score 1005; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-110;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFVILL 60
Db 38 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFVILL 97
QY 61 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYISGGPQEQITVQSWDRKSA 120
Db 98 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYISGGPQEQITVQSWDRKSA 157
QY 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAQLEK 180
Db 158 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAQLEK 217
QY 181 MSEDSCSW 187
Db 218 MSEDSCSW 224

RESULT 4
US-09-242-890-11
; Sequence 11, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
; US-09-242-890-11

Query Match      100.0%; Score 1005; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-110;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFVILL 60
Db 38 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFVILL 97
QY 61 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYISGGPQEQITVQSWDRKSA 120
Db 98 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYISGGPQEQITVQSWDRKSA 157
QY 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAQLEK 180
Db 158 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAQLEK 217
QY 181 MSEDSCSW 187
Db 218 MSEDSCSW 224

RESULT 5
US-10-187-904-2
; Sequence 2, Application US/10187904
; Patent No. 6683161
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403DI
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; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-3

Query Match      87.1%; Score 875; DB 2; Length 187;
Best Local Similarity 84.9%; Pred. No. 2.2e-95;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy  2  PRPCQAPQWEGRQVMYQQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLY 61
Db  2  POPCAAPQWEGRQVLYQQSSGHNRRALVSVDGLNQRVRLDERKALIPCKRLFEYILLY 61
Qy  62  KGVMFQIDQATKQCSKMTLTQPDWDLDPQNSTFEDQYSIGGPQEQITVQWSDRKSAR 121
Db  62  KEGVMFQIEQATKQCAKIPLVESWDPLDPQNSTFEDQYSIGGPQEQILVQWSDRRTAR 121
Qy  122 SYETWIGIYTKDCYPVQETFTTINYSVILSTRPFDIQLGKIDPVSFTPPSTCQMAQLEKM 181
Db  122 SYETWIGVYTKADCPVQETFIRNYTVVMSTRFDDVQLGIDKPSVFTPPSTCQAAQPEKM 181
Qy  182 SEDCS 186
Db  182 SDGCS 186
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```
RESULT 9
US-09-242-890-13
; Sequence 13, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 13
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-13

Query Match      87.1%; Score 875; DB 2; Length 224;
Best Local Similarity 84.9%; Pred. No. 2.9e-95;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy  2  PRPCQAPQWEGRQVMYQQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLY 61
Db  39  POPCAAPQWEGRQVLYQQSSGHNRRALVSVDGLNQRVRLDERKALIPCKRLFEYILLY 98
Qy  62  KGVMFQIDQATKQCSKMTLTQPDWDLDPQNSTFEDQYSIGGPQEQITVQWSDRKSAR 121
Db  99  KEGVMFQIEQATKQCAKIPLVESWDPLDPQNSTFEDQYSIGGPQEQILVQWSDRRTAR 158
```

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Qy  122 SYETWIGIYTKDCYPVQETFTTINYSVILSTRPFDIQLGKIDPVSFTPPSTCQMAQLEKM 181
Db  159 SYETWIGVYTKADCPVQETFIRNYTVVMSTRFDDVQLGIDKPSVFTPPSTCQAAQPEKM 218
Qy  182 SEDCS 186
Db  219 SDGCS 223
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RESULT 10
US-09-242-890-8
; Sequence 8, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like
US-09-242-890-8
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Query Match      20.0%; Score 201; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  31  SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 69
Db  1  SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 39
```

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RESULT 11
US-09-229-583A-4
; Sequence 4, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorphus mykiss
US-09-229-583A-4
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Query Match      18.0%; Score 180.5; DB 2; Length 221;
Best Local Similarity 25.3%; Pred. No. 6e-13;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;
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;
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/Jp97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse ependym
US-09-242-890-5

Query Match      17.4%; Score 175; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      68 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 99
Db      1 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 32

RESULT 14
US-09-229-583A-5
; Sequence 5, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Cyprinus carpio
US-09-229-583A-5

Query Match      16.2%; Score 163; DB 2; Length 215;
Best Local Similarity 24.2%; Pred. No. 6.9e-11;
Matches 47; Conservative 45; Mismatches 84; Indels 18; Gaps 7;

Qy      3 RPOCAPQWEGROVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFEYILY 60
Db      25 QPCHSPLTSG--TKVVSTGGHLAGSEFSYDSKANKRFVEDTAHANKTSHM-DVLVH 81

Qy      61 YKQGMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGG---QEQITVQWSDRK 117
Db      82 FEEGVLVEIDSKNESCKETLQPRKHLMEIIPDATHSEIYMGSPSITEQGLRVRVWNGK 141

Qy      118 ----KSARSYETWIGIYTKDCYPVQETFTINYSVILSTRFEDQLGDKPSVFTPPSTC 173
Db      142 LPELHAHYSLSLST-----TSCGCLFVSGSYGDKDLIFS-FFVETEVDPPQVFPVPAYC 195

Qy      174 QMAQLEKMSDCSW 187
Db      196 EAVAFEEAPDDHSP 209

RESULT 15
US-10-187-904-5

;
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/Jp97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse ependym
US-09-242-890-5

Query Match      17.4%; Score 175; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      68 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 99
Db      1 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 32

RESULT 14
US-09-229-583A-5
; Sequence 5, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorhynchus mykiss
US-10-187-904-4

Query Match      18.0%; Score 180.5; DB 2; Length 221;
Best Local Similarity 25.3%; Pred. No. 6e-13;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;

Qy      2 PRPCAPQWEGROVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILY 61
Db      26 PCHCTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRFTESEMHNLKNTHELDYLMLF 85

Qy      62 KQGMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGG---PQEQITVQWSDRK 118
Db      86 EEGVYDIDMKNQSKCKMSLHSHAHLELPAGAAHQVELFLGSDTVQEDNKKVNIWNG-S 144

Qy      119 SARSYETWIGIYTKDCYPVQETFTINYSVILSTRFEDQLGDKPSVFTPPSTCQMAQL 178
Db      145 VAETKGOYSALTTVGECUPL-STFYSTDSTITLFSNSEVTVTKAPENFTLPSFCEAVEL 203

Qy      179 EK 180
Db      204 EE 205

RESULT 12
US-10-187-904-4
; Sequence 4, Application US/10187904
; Patent No. 6683161
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D1
; CURRENT APPLICATION NUMBER: US/10/187,904
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorhynchus mykiss
US-10-187-904-4

Query Match      18.0%; Score 180.5; DB 2; Length 221;
Best Local Similarity 25.3%; Pred. No. 6e-13;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;

Qy      2 PRPCAPQWEGROVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILY 61
Db      26 PCHCTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRFTESEMHNLKNTHELDYLMLF 85

Qy      62 KQGMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGG---PQEQITVQWSDRK 118
Db      86 EEGVYDIDMKNQSKCKMSLHSHAHLELPAGAAHQVELFLGSDTVQEDNKKVNIWNG-S 144

Qy      119 SARSYETWIGIYTKDCYPVQETFTINYSVILSTRFEDQLGDKPSVFTPPSTCQMAQL 178
Db      145 VAETKGOYSALTTVGECUPL-STFYSTDSTITLFSNSEVTVTKAPENFTLPSFCEAVEL 203

Qy      179 EK 180
Db      204 EE 205

RESULT 13
US-09-242-890-5
; Sequence 5, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:11:35 ; Search time 181 Seconds  
(without alignments)  
478.570 Million cell updates/sec

Title: US-10-733-646-2\_COPY\_38\_224

Perfect score: 1005

Sequence: 1 APRCQAPQWEGRVYQQ.....TPPSTCQMAQLEKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	100.0	187	4	US-10-612-788-1
2	1005	100.0	200	4	US-10-612-788-10
3	1005	100.0	224	4	US-10-612-788-11
4	1005	100.0	224	4	US-10-733-646-2
5	1005	100.0	224	5	US-10-733-646-2
6	886	88.2	190	4	US-10-612-788-2
7	886	88.2	224	4	US-10-612-788-3
8	875	87.1	187	4	US-10-612-788-3
9	875	87.1	224	4	US-10-612-788-13
10	201	20.0	39	4	US-10-612-788-8
11	180.5	18.0	221	4	US-10-733-646-4
12	180.5	18.0	221	5	US-10-733-646-4
13	175	17.4	32	4	US-10-612-788-5
14	163	16.2	215	4	US-10-733-646-5
15	163	16.2	215	5	US-10-733-646-5
16	162	16.1	212	4	US-10-733-646-7
17	162	16.1	212	5	US-10-733-646-7
18	151	15.0	217	4	US-10-733-646-6
19	151	15.0	217	5	US-10-733-646-6
20	148	14.7	216	4	US-10-733-646-3
21	148	14.7	216	5	US-10-733-646-3
22	147	14.6	25	4	US-10-612-788-9
23	143	14.2	25	4	US-10-612-788-6
24	93	9.3	17	4	US-10-612-788-7
25	82	8.1	419	4	US-10-724-972A-5096
26	81	8.1	970	4	US-10-351-157-135
27	81	8.1	970	4	US-10-352-554-120

28	79.5	7.9	2548	3	US-09-851-682A-1	Sequence 1, Appli
29	79	7.9	144	4	US-10-282-122A-71270	Sequence 71270, A
30	78	7.8	13	4	US-10-612-788-4	Sequence 4, Appli
31	78	7.8	1527	4	US-10-437-421-23	Sequence 23, Appli
32	77	7.7	469	4	US-10-166-349-7	Sequence 7, Appli
33	76.5	7.6	405	4	US-10-424-599-229122	Sequence 229122,
34	76.5	7.6	405	6	US-11-188-298-22061	Sequence 1811, A
35	76.5	7.6	896	4	US-10-408-765A-1811	Sequence 22061, A
36	76.5	7.6	923	4	US-10-258-106-7	Sequence 1811, Ap
37	76.5	7.6	950	5	US-10-501-035-357	Sequence 7, Appli
38	76	7.6	1148	3	US-09-949-029-128	Sequence 357, App
39	76	7.6	1148	6	US-11-097-143-9816	Sequence 128, App
40	76	7.6	1302	5	US-10-732-923-1706	Sequence 9816, Ap
41	76	7.6	1431	5	US-10-732-923-1687	Sequence 1706, Ap
42	76	7.6	1490	6	US-11-188-298-4123	Sequence 1687, Ap
43	76	7.6	1500	5	US-10-732-923-1638	Sequence 4123, Ap
44	75.5	7.5	104	4	US-10-437-963-159569	Sequence 1638, Ap
45	75.5	7.5	439	6	US-11-096-568A-30803	Sequence 159569,
						Sequence 30803, A

ALIGNMENTS

RESULT 1

US-10-612-788-1  
; Sequence 1, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-612-788-1

Query Match	100.0%	Score 1005;	DB 4;	Length 187;
Best Local Similarity	100.0%	Pred. No. 8.7e-101;		
Matches 187;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	APRCQAPQWEGRVYQQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILL	60	
Db	1	APRCQAPQWEGRVYQQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILL	60	
Qy	61	YKQWVFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGPQEQITVQWSDRKS	120	
Db	61	YKQWVFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGPQEQITVQWSDRKS	120	
Qy	121	RSVETWIGITVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPFSVFTPPSTCQMAQLEK	180	
Db	121	RSVETWIGITVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPFSVFTPPSTCQMAQLEK	180	
Qy	181	MSEDSCSW 187		
Db	181	MSEDSCSW 187		

RESULT 2

US-10-612-788-10  
; Sequence 10, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro

; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: human  
US-10-612-788-10

Query Match 100.0%; Score 1005; DB 4; Length 200;  
Best Local Similarity 100.0%; Pred. No. 9.5e-101; Indels 0; Gaps 0;  
Matches 187; Conservative 0; Mismatches 0;

Qy 1 APRCPAQWEGQVQWYQSSGNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60  
Db 14 APRCPAQWEGQVQWYQSSGNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 73  
Qy 61 YKGVWFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQSQITVQWSDRKA 120  
Db 74 YKGVWFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQSQITVQWSDRKA 133  
Qy 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAOLEK 180  
Db 134 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAOLEK 193  
Qy 181 MSEDCSW 187  
Db 194 MSEDCSW 200

RESULT 3  
US-10-612-788-11  
; Sequence 11, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: human  
US-10-612-788-11

Query Match 100.0%; Score 1005; DB 4; Length 224;  
Best Local Similarity 100.0%; Pred. No. 1.1e-100;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRCPAQWEGQVQWYQSSGNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60  
Db 38 APRCPAQWEGQVQWYQSSGNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97  
Qy 61 YKGVWFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQSQITVQWSDRKA 120  
Db 98 YKGVWFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQSQITVQWSDRKA 157

Qy 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAOLEK 180  
Db 158 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAOLEK 217  
Qy 181 MSEDCSW 187  
Db 218 MSEDCSW 224

## RESULT 4

US-10-733-646-2  
; Sequence 2, Application US/10733646  
; Publication No. US20040122215A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin  
; FILE REFERENCE: PF403D2  
; CURRENT APPLICATION NUMBER: US/10/733,646  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: US 10/187,904  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 09/229,583  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,330  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: US 60/075,278  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-733-646-2

Query Match 100.0%; Score 1005; DB 4; Length 224;  
Best Local Similarity 100.0%; Pred. No. 1.1e-100;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRCPAQWEGQVQWYQSSGNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60  
Db 38 APRCPAQWEGQVQWYQSSGNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97  
Qy 61 YKGVWFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQSQITVQWSDRKA 120  
Db 98 YKGVWFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQSQITVQWSDRKA 157  
Qy 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAOLEK 180  
Db 158 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPSPVFTPPSTCMAOLEK 217  
Qy 181 MSEDCSW 187  
Db 218 MSEDCSW 224

## RESULT 5

US-10-733-646-2  
; Sequence 2, Application US/10733646  
; Publication No. US20050197491A9  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin  
; FILE REFERENCE: PF403D2  
; CURRENT APPLICATION NUMBER: US/10/733,646  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: US 10/187,904  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 09/229,583  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,330  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: US 60/075,278

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; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 1005; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-100;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRCPAQWEGRVQMYQQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
    |||
Db 38 APRCPAQWEGRVQMYQQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97

Qy 61 YKGVWFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKS 120
    |||
Db 98 YKGVWFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKS 157

Qy 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEK 180
    |||
Db 158 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEK 217

Qy 181 MSEDCSW 187
    |||
Db 218 MSEDCSW 224

RESULT 6
US-10-612-788-2
; Sequence 2, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; PRIOR FILING DATE: 2003-07-02
; PRIOR FILING DATE: 1999-02-25
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-10-612-788-2

Query Match      88.2%; Score 886; DB 4; Length 190;
Best Local Similarity 86.5%; Pred. No. 8e-88;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

Qy 2 PRCPAQWEGRVQMYQQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 61
    |||
Db 5 PQCPAQWEGRVQLYQQSSGHNRALVSVDGLNQRVRLDERKALIPCKRLFEYILL 64

Qy 62 KGVWFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSAR 121
    |||
Db 65 KGVWFQIEQATKCAKIPLAEFPDPLDIPONSTFEDQYSIGGPQEQIMVQWSDRRTAR 124

Qy 122 SYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKM 181
    |||
Db 125 SYETWIGVYAKDCYPVQETFIRNYTVLSTRFFDVQLGIKDPVSFTPPSTCQTAQPEKM 184

Qy 182 SEDCS 186
    |||
Db 185 KENCS 189
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RESULT 7
US-10-612-788-12
; Sequence 12, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; PRIOR FILING DATE: 2003-07-02
; PRIOR FILING DATE: 1999-02-25
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rat
US-10-612-788-12

Query Match      88.2%; Score 886; DB 4; Length 224;
Best Local Similarity 86.5%; Pred. No. 1e-87;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

Qy 2 PRCPAQWEGRVQMYQQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 61
    |||
Db 39 PQCPAQWEGRVQLYQQSSGHNRALVSVDGLNQRVRLDERKALIPCKRLFEYILL 98

Qy 62 KGVWFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSAR 121
    |||
Db 99 KGVWFQIEQATKCAKIPLAEFPDPLDIPONSTFEDQYSIGGPQEQIMVQWSDRRTAR 158

Qy 122 SYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKM 181
    |||
Db 159 SYETWIGVYAKDCYPVQETFIRNYTVLSTRFFDVQLGIKDPVSFTPPSTCQTAQPEKM 218

Qy 182 SEDCS 186
    |||
Db 219 KENCS 223

RESULT 8
US-10-612-788-3
; Sequence 3, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; PRIOR FILING DATE: 2003-07-02
; PRIOR FILING DATE: 1999-02-25
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: mouse
US-10-612-788-3

Query Match      87.1%; Score 875; DB 4; Length 187;
Best Local Similarity 84.9%; Pred. No. 1.2e-86;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy 2 PRCPAQWEGRVQMYQQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 61
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Db 2 POPCQAPQWEGRQVLYQSSGHNRLSYDGLNQRVRLDERKALIPCKRLFYILLY 61  
QY 62 KDGVMFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGGPQOITVQWSDRSAR 121  
Db 62 KEGVMFQIEQATKQCAKIPLVESWDPLDIPONSTFEDQYSIGGPQOILVQWSDRRTAR 121  
QY 122 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQLEKM 181  
Db 122 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQPEKM 181  
QY 182 SEDCS 186  
Db 182 SDGCS 186

RESULT 9  
US-10-612-788-13  
; Sequence 13, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612.788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Mouse  
US-10-612-788-13

Query Match 87.1%; Score 875; DB 4; Length 224;  
Best Local Similarity 84.9%; Pred. No. 1.6e-86;  
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;  
QY 2 PRPCQAPQWEGRQVLYQSSGHNRLSYDGLNQRVRLDERKALIPCKRLFYILLY 61  
Db 39 POPCQAPQWEGRQVLYQSSGHNRLSYDGLNQRVRLDERKALIPCKRLFYILLY 98  
QY 62 KDGVMFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGGPQOITVQWSDRSAR 121  
Db 99 KEGVMFQIEQATKQCAKIPLVESWDPLDIPONSTFEDQYSIGGPQOILVQWSDRRTAR 158  
QY 122 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQLEKM 181  
Db 159 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQPEKM 218  
QY 182 SEDCS 186  
Db 219 SDGCS 223

RESULT 10  
US-10-612-788-8  
; Sequence 8, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612.788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-612-788-8  
Query Match 20.0%; Score 201; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.5e-14;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 SYDGLNQRVRLDERKALIPCKRLFYILLYKDGVMFQI 69  
Db 1 SYDGLNQRVRLDERKALIPCKRLFYILLYKDGVMFQI 39  
RESULT 11  
US-10-733-646-4  
; Sequence 4, Application US/10733646  
; Publication No. US20040122215A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin  
; FILE REFERENCE: PF403D2  
; CURRENT APPLICATION NUMBER: US/10/733.646  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: US 10/187,904  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 09/229,583  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,330  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: US 60/075,278  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Oncomorhynchus mykiss  
US-10-733-646-4  
Query Match 18.0%; Score 180.5; DB 4; Length 221;  
Best Local Similarity 25.3%; Pred. No. 6.1e-11;  
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;  
QY 2 PRPCQAPQWEGRQVLYQSSGHNRLSYDGLNQRVRLDERKALIPCKRLFYILLY 61  
Db 26 PCHCTSPNMTGVLTVMALTGTGGEIKATGHVSYDSTNKKLRFTESEMHJNKTEHLEDYLMLF 85  
QY 62 KDGVMFQIDQATKQCSKMTLTQPWDPLDIPONSTFEDQYSIGG---PQEQITVQWSDRK 118  
Db 86 EGVFYDIDKNQSCCKNLSHSHALELPAGAAHQVELFLGSDTVQEDNIKNINWG-S 144  
QY 119 SARSYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQL 178  
Db 145 VAEKQYSALTTVGECPLP-STFYSTDSTITLLFSNSEVVTEVKAPEMFTLPSPCEAVEL 203  
QY 179 EK 180  
Db 204 EE 205

RESULT 12  
US-10-733-646-4  
; Sequence 4, Application US/10733646  
; Publication No. US20050197491A9  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.  
; TITLE OF INVENTION: Human Ependymin



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; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorhynchus mykiss
US-10-733-646-4

Query Match      18.0%; Score 180.5; DB 5; Length 221;
Best Local Similarity 25.3%; Pred. No. 6.1e-11;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;

Qy  2  PRCPAQPOQWEGRWYQOQSGRNRALLSYDGLNQRVRLDERKALIPCKRLEYILLY 61
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  26  PQHCTSPNMTGVLTMALTGGEIKATGHYSYDSTNKKLRFTESEMHNLKTEHLEDYLM 85
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Qy  62  KGVMPFOIDQATKQCSKMTLTQPDPLDIPQNSTFFDOYSIGG---PQEQITVQWSDRK 118
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  86  EGVFYDIDMKNQSCCKNSLHSHAHLELPAGAAHQVFLFGSTVQEDNKNVIMWG-S 144
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Qy  119  SARYETWIGTYIVKDCVPVQETFTINYSVILSTRFFDIQIGKDPVSFTPPSTCOMAQL 178
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  145  VAETKGOYSALTIVGECPLP-STFYSTDSTILFNSSEVTEVKAPENFTLPSCEAVEL 203
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Qy  179  EK 180
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Db  204  EE 205

RESULT 13
US-10-612-788-5
; Sequence 5, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-5

Query Match      17.4%; Score 175; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  68  QIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQ 99
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  1  QIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQ 32
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 14
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US-10-733-646-5
; Sequence 5, Application US/10733646
; Publication No. US20040122215A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Cyprinus carpio
US-10-733-646-5

Query Match      16.2%; Score 163; DB 4; Length 215;
Best Local Similarity 24.2%; Pred. No. 4.7e-09;
Matches 47; Conservative 45; Mismatches 84; Indels 18; Gaps 7;

Qy  3  RCPQAPQWEGRWYQOQSGRNRALL--LSYDGLNQRVRLDERKALIPCKRLEYILLY 60
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  25  QPCHSPLTSG--TMKVVSITGGHDLASGEFSYDSKANKRFVEDTAHANKTSHM-DVLVH 81
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Qy  61  YKGVMPFOIDQATKQCSKMTLTQPDPLDIPQNSTFFDOYSIGP---QEQITVQWSDRK 117
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  82  FEEGVLYEIDSKNESCKETLQFRKHLMEIPPDATHESEIYMGSPSITEQGLRVRVWNGK 141
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Qy  118  ----KSARYETWIGTYIVKDCVPVQETFTINYSVILSTRFFDIQIGKDPVSFTPPSTC 173
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  142  LPELHAHYSLSLST-----TSCGLPVSYSYVDKKDLIFS-PFGVETEVDQVFPVPAYC 195
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Qy  174  QMAQLEKMSDCSW 187
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  196  EAVAFEEAPDDHSF 209
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 15
US-10-733-646-5
; Sequence 5, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Cyprinus carpio
US-10-733-646-5

Query Match      16.2%; Score 163; DB 5; Length 215;
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:12:30 ; Search time 17 Seconds  
(without alignments)  
139.075 Million cell updates/sec

Title: US-10-733-646-2\_COPY\_38\_224

Perfect score: 1005

Sequence: 1 APRPCAPQWEGRQVMYQQ.....TPPSTCQMAQLKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pdb:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pdb:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pdb:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pdb:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pdb:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pdb:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pdb:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84.5	8.4	931	6 US-10-524-979-2	Sequence 2, Appli
2	69.5	6.9	413	6 US-10-953-349-24222	Sequence 24222, A
3	69.5	6.9	429	6 US-10-953-349-24221	Sequence 24221, A
4	69.5	6.9	431	6 US-10-953-349-24220	Sequence 24220, A
5	69.5	6.9	3882	6 US-10-953-349-5549	Sequence 5549, Ap
6	69.5	6.9	3978	6 US-10-953-349-5548	Sequence 5548, Ap
7	69.5	6.9	4118	6 US-10-953-349-5547	Sequence 5547, Ap
8	69	6.9	802	7 US-11-293-697-3610	Sequence 3610, Ap
9	67.5	6.7	294	6 US-10-953-349-5105	Sequence 5105, Ap
10	67.5	6.7	383	6 US-10-953-349-5104	Sequence 5104, Ap
11	67.5	6.7	439	6 US-10-953-349-5103	Sequence 5103, Ap
12	67.5	6.7	585	7 US-11-293-697-4164	Sequence 4164, Ap
13	66.5	6.6	790	7 US-11-318-939-13	Sequence 13, Appl
14	66	6.6	184	6 US-10-953-349-28907	Sequence 28907, A
15	66	6.6	208	6 US-10-953-349-28906	Sequence 28906, A
16	66	6.6	272	6 US-10-953-349-28905	Sequence 28905, A
17	66	6.6	730	6 US-10-505-928-841	Sequence 841, App
18	65.5	6.5	1871	6 US-10-501-834-26	Sequence 26, Appl
19	65	6.5	695	7 US-11-293-697-4190	Sequence 4190, Ap
20	64.5	6.4	911	7 US-11-313-450-25	Sequence 25, Appl
21	64	6.4	274	7 US-11-293-697-4076	Sequence 4076, Ap
22	64	6.4	362	7 US-11-293-697-2645	Sequence 2645, Ap
23	63.5	6.3	453	6 US-10-471-571A-1056	Sequence 1056, Ap
24	63	6.3	847	6 US-10-505-928-495	Sequence 495, App
25	62.5	6.2	208	6 US-10-953-349-30987	Sequence 30987, A

ALIGNMENTS

RESULT 1

US-10-524-979-2  
; Sequence 2, Application US/10524979  
; Publication No. US20060094013A1  
; GENERAL INFORMATION:  
; APPLICANT: Takemori, Hiroshi  
; TITLE OF INVENTION: SALT-INDUCIBLE KINASE 2 AND USE THEREOF  
; FILE REFERENCE: WATA-003  
; CURRENT APPLICATION NUMBER: US/10/524,979  
; PRIOR FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: 2002-240092  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: 2003-23295  
; PRIOR FILING DATE: 2003-01-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 931  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-524-979-2

Query Match 8.4%; Score 84.5; DB 6; Length 931;  
Best Local Similarity 22.9%; Pred. No. 0.62;  
Matches 57; Conservative 33; Mismatches 80; Indels 79; Gaps 14;  
QY 4 PCQAPQWEGRQ-----VMYQSSGSRNALLSYDG-----LNQRRVLDER 45  
DB 181 PYAAPEVEGQYEGPQDLINSMGVLYLVLCG-----ALPDPGPTLPIRQRLV---EG 232  
QY 46 KALIP-----CKELFEVILLYKGVMEQIDQATKQCSKMTLTQPWD-PLDIPQNSTFED 98  
DB 233 RFRIPYFMSEDCHEILRRMLVLDPSKRLSIAQ-IKEHKWMLIEVPVQRPILYPQSQ--EN 289  
QY 99 QYSIGGGPQEQ-----ITVQWSDRKSARSYETWIGIVTV-----KDCYPVQST 141  
DB 290 EPSIGEFNEQVLRMLHSLGIDQKTVESLQNSYNHFAIIFLLVERLKSRRSFPVEQR 349  
QY 142 F-----TTNYSVILSTRFFDIQLGIKDPVS-----FT-PPSTCQMA 176  
DB 350 LDGRRQRPSTIAEQTVAKAQTVGLPVTLHPNPNVLRMLRSTLLPQASNVFAFSPTSSCQ-A 408  
QY 177 QLEKMSDC 185  
DB 409 EAAPMEBEC 417

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RESULT 2
US-10-953-349-24222
; Sequence 24222, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24222
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24222
Query Match 6.9%; Score 69.5; DB 6; Length 413;
Best Local Similarity 21.1%; Pred. No. 8;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;

Qy 13 GROWMYQSSGRNSRALLSY-----DGLNQRRVRLDERKALIPCKRLFEYILLY 61
Db 38 GGOVIYSGPLGRNSHKIVEFEAIPGVPKIKEMYNPATWMLLEVSSVAEVRGLGMDFAEY 97
Qy 62 KDGVMFOIDQA-TKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWMSDRKSA 120
Db 98 KTSLSLFRNKALVKELS-----TPPGATDL-----YFPTKYS-----QSTLGQF---KSC 140
Qy 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGDKPS-----VF 167
Db 141 -FWKQWLTWYRSPDYNLVRYFFTLACALMIGTVFWRIGKKNRESSADLTMIIGAMYAAVIF 199
Qy 168 TPSTCQMAQ 177
Db 200 VGINNCQTVQ 209

RESULT 3
US-10-953-349-24221
; Sequence 24221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24221
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24221
Query Match 6.9%; Score 69.5; DB 6; Length 429;
Best Local Similarity 21.1%; Pred. No. 8.4;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;

Qy 13 GROWMYQSSGRNSRALLSY-----DGLNQRRVRLDERKALIPCKRLFEYILLY 61
Db 54 GGOVIYSGPLGRNSHKIVEFEAIPGVPKIKEMYNPATWMLLEVSSVAEVRGLGMDFAEY 113
Qy 62 KDGVMFOIDQA-TKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWMSDRKSA 120
Db 114 KTSLSLFRNKALVKELS-----TPPGATDL-----YFPTKYS-----QSTLGQF---KSC 156
Qy 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGDKPS-----VF 167
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Db 157 -FWKQWLTWYRSPDYNLVRYFFTLACALMIGTVFWRIGKKNRESSADLTMIIGAMYAAVIF 215
Qy 168 TPSTCQMAQ 177
Db 216 VGINNCQTVQ 225

RESULT 4
US-10-953-349-24220
; Sequence 24220, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24220
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24220
Query Match 6.9%; Score 69.5; DB 6; Length 431;
Best Local Similarity 21.1%; Pred. No. 8.4;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;

Qy 13 GROWMYQSSGRNSRALLSY-----DGLNQRRVRLDERKALIPCKRLFEYILLY 61
Db 56 GGOVIYSGPLGRNSHKIVEFEAIPGVPKIKEMYNPATWMLLEVSSVAEVRGLGMDFAEY 115
Qy 62 KDGVMFOIDQA-TKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWMSDRKSA 120
Db 116 KTSLSLFRNKALVKELS-----TPPGATDL-----YFPTKYS-----QSTLGQF---KSC 158
Qy 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGDKPS-----VF 167
Db 159 -FWKQWLTWYRSPDYNLVRYFFTLACALMIGTVFWRIGKKNRESSADLTMIIGAMYAAVIF 217
Qy 168 TPSTCQMAQ 177
Db 218 VGINNCQTVQ 227

RESULT 5
US-10-953-349-5549
; Sequence 5549, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5549
; LENGTH: 3882
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5549
Query Match 6.9%; Score 69.5; DB 6; Length 3882;
Best Local Similarity 24.1%; Pred. No. 1.3e+02;
Matches 52; Conservative 34; Mismatches 71; Indels 59; Gaps 16;

Qy 1 APRPCQ-APQOWEGRQ--VMY--QOSSGRNSR-----ALLSYDGLNQRRVRLD-ERKALI 49
Db 2992 SPWPSMLSPQESAGRSQVLFPSQKDSVSPRIGIAVAARDSVSPGISLLELEKKERI 3051
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Query Match 6.7%; Score 67.5; DB 6; Length 294;
Best Local Similarity 19.4%; Pred. No. 8.4;
Matches 38; Conservative 28; Mismatches 57; Indels 73; Gaps 9;

QY 15 QVMYQSSGRNRALLSYDGL-----NORVRVLDERKALIPCKRLFEYILLYK----- 62
Db 46 KVMWGESSMIEAERLLASALEHNSQRFVLLSDR-----CAPLYDFGIYKYLLISSPRS 100
QY 63 -----DGVMFQI-DQATKQC 76
Db 101 FVDSFLHTKETRYSVKMSVPIPEEKWRKGSQWIALIRSHAENVINDGIVFPVPEKFCRC 160
QY 77 SKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRSAR--SYETW--IGI-YT 131
Db 161 PPLGTNEAMLFLKQKRRNCIPDEHYV---QTLTLMQGLESEMERTVTYTVNVNVSCTKYE 217
QY 132 VKDCYPVQETFTINYS 147
Db 218 AKSWHPV--TFTLENS 231

RESULT 10
US-10-953-349-5104
; Sequence 5104, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5104
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5104

Query Match 6.7%; Score 67.5; DB 6; Length 383;
Best Local Similarity 19.4%; Pred. No. 12;
Matches 38; Conservative 28; Mismatches 57; Indels 73; Gaps 9;

QY 15 QVMYQSSGRNRALLSYDGL-----NORVRVLDERKALIPCKRLFEYILLYK----- 62
Db 135 KVMWGESSMIEAERLLASALEHNSQRFVLLSDR-----CAPLYDFGIYKYLLISSPRS 189
QY 63 -----DGVMFQI-DQATKQC 76
Db 190 FVDSFLHTKETRYSVKMSVPIPEEKWRKGSQWIALIRSHAENVINDGIVFPVPEKFCRC 249
QY 77 SKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRSAR--SYETW--IGI-YT 131
Db 250 PPLGTNEAMLFLKQKRRNCIPDEHYV---QTLTLMQGLESEMERTVTYTVNVNVSCTKYE 306
QY 132 VKDCYPVQETFTINYS 147
Db 307 AKSWHPV--TFTLENS 320

RESULT 11
US-10-953-349-5103
; Sequence 5103, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5103
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5103

Query Match 6.7%; Score 67.5; DB 6; Length 439;
Best Local Similarity 19.4%; Pred. No. 14;
Matches 38; Conservative 28; Mismatches 57; Indels 73; Gaps 9;

QY 15 QVMYQSSGRNRALLSYDGL-----NORVRVLDERKALIPCKRLFEYILLYK----- 62
Db 191 KVMWGESSMIEAERLLASALEHNSQRFVLLSDR-----CAPLYDFGIYKYLLISSPRS 245
QY 63 -----DGVMFQI-DQATKQC 76
Db 246 FVDSFLHTKETRYSVKMSVPIPEEKWRKGSQWIALIRSHAENVINDGIVFPVPEKFCRC 305
QY 77 SKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRSAR--SYETW--IGI-YT 131
Db 306 PPLGTNEAMLFLKQKRRNCIPDEHYV---QTLTLMQGLESEMERTVTYTVNVNVSCTKYE 362

RESULT 12
US-11-293-697-4164
; Sequence 4164, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: HL-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4164
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4164

Query Match 6.7%; Score 67.5; DB 7; Length 585;
Best Local Similarity 20.0%; Pred. No. 20;
Matches 30; Conservative 28; Mismatches 51; Indels 41; Gaps 6;

QY 36 NORVRVLDERKALIPCKRLF--EYILLYKDGVMFQIDQATKQCSKMT-----LTQP 84
Db 195 HQTQKIEKPHACIECEQTFLRKSQLIYHENICIQENPGSGQCEKLSRVLFTHKPKTNT 254
QY 85 WDLPLDIPQNSTFEDQYSIGGPQEQITV---QEWSDRSARSYETWICI----- 129
Db 255 TDKICIP-----NEVRKGSVTKSSLTHQOHTTEKSYMCEGCGKGTMKRYLIAHQRT 308
QY 130 -----YTVKDCYPVQETFTINYSVILSTR 153
Db 309 HSGEKPYVCKEC---GKGFTVKSNLIVHOR 335

RESULT 13
US-11-318-939-13
; Sequence 13, Application US/11318939
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Soff, Gerald
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
```



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CC endodymin activity. Human endodymin can be used to treat conditions in  
CC patients having need of the endodymin protein. Conditions that can be  
CC treated or detected are nervous system-related disorders, such as  
CC Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis,  
CC pain, stroke, depression, anxiety, epilepsy and other neurological or  
CC psychiatric disorders. Diagnosis of cancers of the nervous system is also  
CC included. Endodymin, or its agonists or antagonists may also be used to  
CC treat disorders of the blood-brain barrier since endodymin participates  
CC in the endothelial cell barrier by modulating cell-matrix interactions.  
CC Antagonists may inhibit formation of endodymin-collagen fibrils, which  
CC cover endothelial cells of numerous blood vessels, hence anti-endodymin  
CC antibodies may regulate angiogenesis

XX SQ Sequence 224 AA;

Query Match 100.0%; Score 224; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 2.5e-216;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPCRPLRTVPGALGAWLLGGLWANTLCGLCSLGVAGVAPRCPQAPQWEGRVMYQSSG 60  
DB 1 MPCRPLRTVPGALGAWLLGGLWANTLCGLCSLGVAGVAPRCPQAPQWEGRVMYQSSG 60  
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120  
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120  
QY 121 PWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIVTKDCYPVQETFT 180  
DB 121 PWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIVTKDCYPVQETFT 180  
QY 181 INYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224  
DB 181 INYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224

RESULT 3

ID AAY94654  
XX AAY94654 standard; protein; 224 AA.

AC AAY94654;

DT 29-AUG-2000 (first entry)

XX Human homology to endodymin-like protein (HELP) amino acid sequence.

XX Homology to endodymin-like protein; HELP; chromosome 7p14-12;  
KW central nervous system disorder; peripheral nervous system disorder;  
KW Alzheimer's disease; memory loss; stroke; neuronal damage;  
KW osteoblast differentiation; proliferation; stimulation; bone wear;  
KW arthritis; osteoporosis; cerebral cavernous malformation;  
KW Charcot-Marie-Tooth syndrome; human; netrin like protein; NEL.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Peptide 1..37

FT Protein /label= Putative signal peptide

FT Protein 38..224

FT Protein /label= Homology to endodymin-like protein

XX WO200032746-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028341.

XX 30-NOV-1998; 98US-00201442.

XX (MILL-) MILLENNIUM PHARM INC.

XX Pan Y;

DR WPI; 2000-412299/35.  
DR N-PSDB; AAA27982.

XX New nucleic acid molecules, designated NEL, useful for treating  
PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and  
PT neuronal damage (e.g. stroke).

XX PS Claim 9; Fig 4; 97pp; English.

XX This sequence represents a human homology to endodymin-like protein  
CC (HELP) amino acid sequence. Endodymin is a protein that is involved in  
CC memory and neuronal regeneration. The human HELP gene is located on  
CC chromosome 7p14-12. Northern analysis of HELP expression showed that an  
CC approximately 3kb HELP transcript is expressed in the brain, heart, and  
CC skeletal muscle. HELP is a secreted protein. Modulators of HELP  
CC expression or activity can be used to treat disorders of the central  
CC nervous system or peripheral nervous system, e.g. neuronal disorders,  
CC memory associated disorders, such as Alzheimer's disease or stroke, or to  
CC treat neuronal damage. HELP polypeptides, nucleic acids and modulators of  
CC HELP expression or activity may be useful for modulation of osteoblast  
CC differentiation, stimulation or proliferation. They may also be used to  
CC treat cartilage or bone wearing, arthritis or osteoporosis, disorders  
CC such as cerebral cavernous malformation and Charcot-Marie-Tooth disease.  
CC The present invention also relates to a secreted protein with homology to  
CC netrin, called netrin like protein or NEL. NEL is also referred to as  
CC TANGO 205 or T205. Netrin is a chemoattractant. Biological activities of  
CC NEL include interacting with the protein encoded by deleted in colorectal  
CC cancer, modulation of axon growth, migration and development, modulation  
CC of development of the nervous system, and modulation of the guidance of  
CC central nervous system commissural axons and peripheral motor axons

XX SQ Sequence 224 AA;

Query Match 100.0%; Score 224; DB 3; Length 224;  
Best Local Similarity 100.0%; Pred. No. 2.5e-216;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWANTLCGLCSLGVAGVAPRCPQAPQWEGRVMYQSSG 60

DB 1 MPCRPLRTVPGALGAWLLGGLWANTLCGLCSLGVAGVAPRCPQAPQWEGRVMYQSSG 60

QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120

DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120

QY 121 PWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIVTKDCYPVQETFT 180

DB 121 PWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIVTKDCYPVQETFT 180

QY 181 INYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224

DB 181 INYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224

RESULT 4

ADY18068

ID ADY18068 standard; protein; 344 AA.

XX ADY18068;

XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 3874.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

```
XX PD 24-FEB-2005.
XX PF
XX PF
XX PF
XX PR 11-AUG-2004; 2004WO-US026249.
XX PR 11-AUG-2003; 2003US-0493546P.
XX PA (GETH ) GENENTECH INC.
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX PI WPI; 2005-182330/19.
XX DR
XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX PT treating an immune related disorder, e.g. systemic lupus erythematosus,
XX PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX PS Claim 8; SEQ ID NO 3874; 158pp; English.
XX CC The invention relates to an isolated nucleic acid encoding a PRO
XX CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX CC composition, and method are useful for diagnosing and treating an immune
XX CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX CC arthritis. The present sequence represents a PRO polypeptide.
XX SQ Sequence 344 AA;
XX
XX Query Match 100.0%; Score 224; DB 9; Length 344;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-216;
XX Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVYQSSG 60
DB 121 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVYQSSG 180
QY 61 RNSRALLSYDGLNQRVRLDERKALPCKRLFYILLYKDVGMFOIDQATKQCKRWLTQ 120
DB 181 RNSRALLSYDGLNQRVRLDERKALPCKRLFYILLYKDVGMFOIDQATKQCKRWLTQ 240
QY 121 PWDPLDIPQNSTFEDQVSIQGPQEQITVQWSDRKARSYETWIGYTVKDCYPVQETFT 180
DB 241 PWDPLDIPQNSTFEDQVSIQGPQEQITVQWSDRKARSYETWIGYTVKDCYPVQETFT 300
QY 181 INYSVILSTRFFDIQGIKDPVSFTPTSTCQMAQLEKMSDCSW 224
DB 301 INYSVILSTRFFDIQGIKDPVSFTPTSTCQMAQLEKMSDCSW 344
XX
RESULT 5
ABR40123
ID ABR40123 standard; protein; 210 AA.
XX
AC ABR40123;
XX
XX
DT 04-JUL-2003 (first entry)
XX
DE Human cell adhesion and extracellular matrix protein, CADECM-20.
XX
XX Human; anti-HIV; anti-allergic; cerebroprotective; antiparkinsonian;
XX anticonvulsant; neurotropic; neuroprotective; immunosuppressive;
XX dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
XX gene therapy; cell adhesion; extracellular matrix; CADECM;
XX immune system disorder; AIDS; allergy; neurological disorder; stroke;
XX Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
XX cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
XX genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
XX atherosclerosis.
XX
XX Homo sapiens.
OS
XX WO2003027230-A2.
XX
XX 03-APR-2003.
PD
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XX 02-AUG-2002; 2002WO-US024649.
XX PF
XX PF
XX PF
XX PR 03-AUG-2001; 2001US-0309964P.
XX PR 03-AUG-2001; 2001US-0310119P.
XX PR 17-AUG-2001; 2001US-0313091P.
XX PR 31-AUG-2001; 2001US-0316771P.
XX PR 07-SEP-2001; 2001US-0317896P.
XX PR 21-SEP-2001; 2001US-0324781P.
XX PR 05-OCT-2001; 2001US-0327606P.
XX PR 12-OCT-2001; 2001US-0328960P.
XX PR 09-NOV-2001; 2001US-0344471P.
XX PR 17-MAY-2002; 2002US-0381291P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
XX Forsythe IJ, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
XX Kallick DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
XX Wallia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
XX WPI; 2003-354645/33.
XX DR N-PSDB; ACC00411.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
XX PT useful for diagnosing, treating or preventing disorders associated with
XX PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
XX PT or stroke.
XX PS Claim 1; Page 203; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX CC and proteins are useful in diagnosing, treating and preventing disorders
XX CC associated with aberrant expression of CADECM, such as immune system
XX CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX CC proliferative disorders (e.g. cancer or atherosclerosis)
XX SQ Sequence 210 AA;
XX
XX Query Match 40.2%; Score 90; DB 6; Length 210;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-81;
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVYQSSG 60
DB 121 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVYQSSG 180
QY 61 RNSRALLSYDGLNQRVRLDERKALPCKR 90
DB 181 RNSRALLSYDGLNQRVRLDERKALPCKR 210
XX
XX RESULT 6
XX AAWS1120
XX ID AAWS1120 standard; protein; 224 AA.
XX
XX AC AAWS1120;
XX
XX 06-NOV-1998 (first entry)
XX
XX Rat ependymin-like protein.
XX
XX Rat ependymin-like protein; prophylactic agent; Alzheimer's disease;
XX KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
XX KW dementia; cerebellar degeneration; central nervous system; gliocyte;
XX KW memory; neuron.
XX
XX OS Rattus sp.
```

XX	Key	Location/Qualifiers	
PH	Peptide	1. .34	
FT		/note= "Signal peptide; This sequence is claimed by the inventors under claim 10 in the specification"	
FT	Protein	35. .224	
FT		/note= "Rat ependymin-like protein; This sequence is claimed by the inventors under claim 2 in the specification"	
XX	WO9811130-A2.		
PN			
XX	19-MAR-1998.		
PD			
XX	10-SEP-1997;	97WO-JP003194.	
XX			
XX	11-SEP-1996;	96JP-00240880.	
PR			
XX	28-NOV-1996;	96JP-00318049.	
PR			
XX	27-MAY-1997;	97JP-00135633.	
XX			
XX	(TAKE ) TAKEDA CHEM IND LTD.		
XX			
PI	Ogi K, Onda H;		
XX			
DR	WPI; 1998-250952/22.		
DR	N-PSDE; AAV07201.		
XX			
PT	New isolated ependymin-like protein - used to develop products for treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia or cerebellar degeneration.		
PT			
XX	Claim 2, 9, 10; Fig 2A-2C; 147pp; English.		
XX			
CC	The present sequence represents the rat ependymin-like protein. The invention also claims for the human ependymin-like protein (AAW51119) and its corresponding cDNA (AAV07200), and the mouse ependymin-like protein (AAW51121) and its corresponding cDNA (AAV07202). The ependymin-like proteins of the invention are claimed to have nerve-extending activity, neuro-regenerative activity in the central nervous system, gliocyte stimulating activity or memory forming activity. These ependymin-like proteins and the corresponding DNA sequences which encode them are also claimed to be useful as therapeutic or prophylactic agents for Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, dementia or cerebellar degeneration		
XX			
SQ	Sequence 224 AA;		
	Query Match	17.4%; Score 39; DB 2; Length 224;	
	Best Local Similarity	100.0%; Pred. No. 2.1e-30;	
	Matches 39; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	68 SYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQI 106		
Db	68 SYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQI 106		
RESULT 7			
AAW51121			
ID	AAW51121 standard; protein; 224 AA.		
XX			
AC	AAW51121;		
XX			
DT	06-NOV-1998 (first entry)		
XX			
DE	Mouse ependymin-like protein.		
XX			
KW	Mouse ependymin-like protein; prophylactic agent; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; dementia; cerebellar degeneration; central nervous system; gliocyte; memory; neuron.		
KW			
XX			
OS	Mus sp.		
XX			

FH Key Location/Qualifiers  
 FT Peptide 1. .37  
 FT /label= Putative signal peptide  
 FT Protein 38. .224  
 FT /label= Homology to ependymin-like protein  
 XX  
 PN WO200032746-A2.  
 XX  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US028341.  
 XX  
 PR 30-NOV-1998; 98US-00201442.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Pan Y;  
 XX  
 DR WPI; 2000-412299/35.  
 DR N-PSDB; AAA27983.  
 XX  
 PT New nucleic acid molecules, designated NEL, useful for treating  
 PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and  
 PT neuronal damage (e.g. stroke).  
 XX  
 PS Claim 9; Fig 3; 97pp; English.  
 XX  
 CC This sequence represents a mouse homology to ependymin-like protein  
 CC (HELP) amino acid sequence. Ependymin is a protein that is involved in  
 CC memory and neuronal regeneration. HELP is a secreted protein. Northern  
 CC analysis of HELP expressed in the brain, heart, and skeletal muscle. HELP is  
 CC transcript is expressed in the brain, heart, and skeletal muscle. HELP is  
 CC expressed in a punctate manner throughout adult mouse brain, suggesting  
 CC that it is expressed by neurons, it is also expressed in the membrane  
 CC surrounding the placenta. Modulators of HELP expression or activity can  
 CC be used to treat disorders of the central nervous system or peripheral  
 CC nervous system, e.g. neuronal disorders, memory associated disorders,  
 CC such as Alzheimer's disease or stroke, or to treat neuronal damage. HELP  
 CC polypeptides, nucleic acids and modulators of HELP expression or activity  
 CC may be useful for modulation of osteoblast differentiation, stimulation  
 CC or proliferation. They may also be used to treat cartilage or bone  
 CC wearing arthritis or osteoporosis, disorders such as cerebral cavernous  
 CC malformation and Charcot-Marie-Tooth disease. The present invention also  
 CC relates to a secreted protein with homology to netrin, called netrin like  
 CC protein or NEL. NEL is also referred to as TANGO 205 or T205. Netrin is a  
 CC chemoattractant. Biological activities of NEL include interacting with  
 CC the protein encoded by deleted in colorectal cancer, modulation of axon  
 CC growth, migration and development, modulation of development of the  
 CC nervous system, and modulation of the guidance of central nervous system  
 CC commissural axons and peripheral motor axons  
 XX  
 SQ Sequence 224 AA;  
 Query Match 14.3%; Score 32; DB 3; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-23;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 68 SYDGLNQRVRLDERKALIPCKRLFVILLYK 99  
 |||||  
 DB 68 SYDGLNQRVRLDERKALIPCKRLFVILLYK 99  
 |||||  
 RESULT 9  
 AAE07249  
 ID AAE07249 standard; peptide; 8 AA.  
 XX  
 AC AAE07249;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DT  
 XX Peptide #14 used for counteracting effects of ROS and free radicals.  
 DE  
 XX Antioxidative enzyme; catalase; CAT; superoxide dismutase; SOD; therapy;  
 KW

KW reactive oxygen species; ROS; free radical; dietary supplement; stroke;  
 KW AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;  
 KW myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;  
 KW trauma; premature aging; neurodegenerative disease; Tardive dyskinesia;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;  
 KW arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;  
 KW senility; Down's syndrome; macular degeneration; septic shock; epilepsy;  
 KW polytraumatic shock; schizophrenia; antiulcer; clozapine; Huntington's disease;  
 KW cardiant; cerebroprotective; vulnerary; nootropic; Huntington's disease;  
 KW anticonvulsant; neuroprotective; antiarthritis; antiinflammatory; burn;  
 KW cytostatic; leukaemia; ophthalmological; antibacterial;  
 KW immunosuppressive.  
 XX Synthetic.  
 OS  
 XX WO200136454-A1.  
 PN  
 XX 25-MAY-2001.  
 PD  
 XX 17-NOV-2000; 2000WO-US031764.  
 PF  
 XX 18-NOV-1999; 99US-0166381P.  
 PR  
 XX (CERE-) CEREMEDIX INC.  
 PA  
 XX Shashoua VE;  
 PI  
 XX WPI; 2001-496512/54.  
 DR  
 XX Novel peptide compound that up regulates expression of a gene encoding  
 PT antioxidative enzymes, used to treat or prevent conditions caused by  
 PT undesirable elevation of reactive oxygen species and other free radicals.  
 XX  
 PS Claim 19; Page 66; 102pp; English.  
 XX  
 CC The invention relates to peptide compounds and methods for upregulating  
 CC expression of a gene encoding an antioxidative enzyme, such as catalase  
 CC (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative  
 CC effects of reactive oxygen species (ROS) and other free radicals. The  
 CC peptides are used as components of pharmaceuticals and dietary  
 CC supplements. The peptides are used to treat or to prevent diseases and  
 CC conditions characterized by undesirable elevation of ROS and other free  
 CC radicals, to upregulate AP-1 transcription factor gene expression and to  
 CC treat pain. The disease or conditions include renal reperfusion damage, and  
 CC cerebral ischaemia (stroke), myocardial infarction (heart attack), head  
 CC trauma, atherosclerosis, brain trauma, oxygen toxicity in premature  
 CC infants, premature aging, spinal cord trauma, neurodegenerative diseases,  
 CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,  
 CC ulcerative colitis, human leukaemia and other cancers characterised by  
 CC elevation of ROS or free radicals, age-related elevation of ROS or free  
 CC radicals, senility, Down's syndrome, macular degeneration, cataracts,  
 CC septic shock, polytraumatic shock, schizophrenia, burn injuries,  
 CC epilepsy, radiation and/or drug-induced elevation of ROS and free  
 CC radicals, where the drug is a neuroleptic or a drug such as clozapine  
 CC defined in the specification and Tardive dyskinesia. The present sequence  
 CC is a peptide used for counteracting effects of ROS and free radicals  
 XX  
 SQ Sequence 8 AA;  
 Query Match 3.6%; Score 8; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 136 QYSIGGPQ 143  
 |||||  
 DB 1 QYSIGGPQ 8  
 |||||  
 RESULT 10  
 AAE07246  
 ID AAE07246 standard; peptide; 8 AA.  
 XX

AC AAE07246;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Peptide #11 used for counteracting effects of ROS and free radicals.  
XX  
KW Antioxidative enzymes; catalase; CAT; superoxide dismutase; SOD; therapy;  
KW reactive oxygen species; ROS; free radical; dietary supplement; stroke;  
KW AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;  
KW myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;  
KW trauma; premature aging; neurodegenerative disease; tardive dyskinesia;  
KW Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;  
KW arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;  
KW senility; Down's syndrome; macular degeneration; septic shock; epilepsy;  
KW polytraumatic shock; schizophrenia; antiulcer; clozapine; tranquillisers;  
KW cardiant; cerebroprotective; vulnerable; nootropic; Huntington's disease;  
KW anticonvulsant; neuroprotective; antiarthritic; antiinflammatory; burn;  
KW cytostatic; leukaemia; ophthalmological; antibacterial;  
KW immunosuppressive.  
XX  
OS Synthetic.  
XX  
PN W0200136454-A1.  
XX  
PD 25-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-US031764.  
XX  
PP 18-NOV-1999; 99US-0166381P.  
XX  
PR (CERE-) CEREMEDIX INC.  
XX  
PA Shashoua VE;  
XX  
PI WPI; 2001-496512/54.  
XX  
DR Novel peptide compound that up regulates expression of a gene encoding  
XX PT antioxidant enzymes, used to treat or prevent conditions caused by  
XX PT undesirable elevation of reactive oxygen species and other free radicals.  
XX  
PS Claim 8; Page 64; 102pp; English.  
XX  
CC The invention relates to peptide compounds and methods for upregulating  
CC expression of a gene encoding an antioxidative enzyme, such as catalase  
CC (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative  
CC effects of reactive oxygen species (ROS) and other free radicals. The  
CC peptides are used as components of pharmaceuticals and dietary  
CC supplements. The peptides are used to treat or to prevent diseases and  
CC conditions characterised by undesirable elevation of ROS and other free  
CC radicals, to upregulate AP-1 transcription factor gene expression and to  
CC treat pain. The disease or conditions include renal reperfusion damage,  
CC cerebral ischaemia (stroke), myocardial infarction (heart attack), head  
CC trauma, atherosclerosis, brain trauma, oxygen toxicity in premature  
CC infants, premature aging, spinal cord trauma, neurodegenerative diseases,  
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,  
CC ulcerative colitis, human leukaemia and other cancers characterised by  
CC elevation of ROS or free radicals, age-related elevation of ROS or free  
CC radicals, senility, Down's syndrome, macular degeneration, cataracts,  
CC septic shock, polytraumatic shock, schizophrenia, burn injuries,  
CC epilepsy, radiation and/or drug-induced elevation of ROS and free  
CC radicals, where the drug is a neuroleptic or a drug such as clozapine  
CC defined in the specification and Tardive dyskinesia. The present sequence  
CC is a peptide used for counteracting effects of ROS and free radicals.  
CC Note: This sequence SEQ.ID.NO.11 is incorrectly designated as  
CC SEQ.ID.NO.12 in the sequence listing  
XX  
SQ Sequence 8 AA;  
  
Query Match 3.6%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
AC AAE07246;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Peptide #11 used for counteracting effects of ROS and free radicals.  
XX  
KW Antioxidative enzymes; catalase; CAT; superoxide dismutase; SOD; therapy;  
KW reactive oxygen species; ROS; free radical; dietary supplement; stroke;  
KW AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;  
KW myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;  
KW trauma; premature aging; neurodegenerative disease; tardive dyskinesia;  
KW Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;  
KW arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;  
KW senility; Down's syndrome; macular degeneration; septic shock; epilepsy;  
KW polytraumatic shock; schizophrenia; antiulcer; clozapine; tranquillisers;  
KW cardiant; cerebroprotective; vulnerable; nootropic; Huntington's disease;  
KW anticonvulsant; neuroprotective; antiarthritic; antiinflammatory; burn;  
KW cytostatic; leukaemia; ophthalmological; antibacterial;  
KW immunosuppressive.  
XX  
OS Synthetic.  
XX  
PN W0200136454-A1.  
XX  
PD 25-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-US031764.  
XX  
PP 18-NOV-1999; 99US-0166381P.  
XX  
PR (CERE-) CEREMEDIX INC.  
XX  
PA Shashoua VE;  
XX  
PI WPI; 2001-496512/54.  
XX  
DR Novel peptide compound that up regulates expression of a gene encoding  
XX PT antioxidant enzymes, used to treat or prevent conditions caused by  
XX PT undesirable elevation of reactive oxygen species and other free radicals.  
XX  
PS Claim 8; Page 64; 102pp; English.  
XX  
CC The invention relates to peptide compounds and methods for upregulating  
CC expression of a gene encoding an antioxidative enzyme, such as catalase  
CC (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative  
CC effects of reactive oxygen species (ROS) and other free radicals. The  
CC peptides are used as components of pharmaceuticals and dietary  
CC supplements. The peptides are used to treat or to prevent diseases and  
CC conditions characterised by undesirable elevation of ROS and other free  
CC radicals, to upregulate AP-1 transcription factor gene expression and to  
CC treat pain. The disease or conditions include renal reperfusion damage,  
CC cerebral ischaemia (stroke), myocardial infarction (heart attack), head  
CC trauma, atherosclerosis, brain trauma, oxygen toxicity in premature  
CC infants, premature aging, spinal cord trauma, neurodegenerative diseases,  
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,  
CC ulcerative colitis, human leukaemia and other cancers characterised by  
CC elevation of ROS or free radicals, age-related elevation of ROS or free  
CC radicals, senility, Down's syndrome, macular degeneration, cataracts,  
CC septic shock, polytraumatic shock, schizophrenia, burn injuries,  
CC epilepsy, radiation and/or drug-induced elevation of ROS and free  
CC radicals, where the drug is a neuroleptic or a drug such as clozapine  
CC defined in the specification and Tardive dyskinesia. The present sequence  
CC is a peptide used for counteracting effects of ROS and free radicals.  
CC Note: This sequence SEQ.ID.NO.11 is incorrectly designated as  
CC SEQ.ID.NO.12 in the sequence listing  
XX  
SQ Sequence 8 AA;  
  
Query Match 3.6%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 SKMTLTOP 121  
DB 1 SKMTLTOP 8  
  
RESULT 11  
ADJ59106  
ID ADJ59106 standard; peptide; 8 AA.  
AC ADJ59106;  
XX  
DT 06-MAY-2004 (first entry)  
XX Peptide useful for up-regulating telomerase expression.  
XX Telomerase; vulnery.  
XX Synthetic.  
XX OS  
XX W02003066814-A2.  
XX  
PD 14-AUG-2003.  
XX  
PF 03-FEB-2003; 2003WO-US003425.  
XX  
PP 04-FEB-2002; 2002US-0354423P.  
XX  
PR (CERE-) CEREMEDIX INC.  
XX  
PI Adams DS, Shashoua VE;  
XX WPI; 2003-748118/70.  
XX  
PT Upregulating telomerase expression in a eukaryotic cell, tissue or organ  
XX useful for diagnosing and treating degenerative diseases, trauma, or in  
XX prolonging the aging process, comprises using peptide compositions.  
XX Disclosure; SEQ ID NO 19; 72pp; English.  
XX  
CC The present sequence is that of a peptide that is used in a method of the  
CC invention for up-regulating telomerase expression in a eukaryotic cell,  
CC tissue or organ. The method involves contacting the eukaryotic cell,  
CC tissue or organ with the peptide in an amount effective to up-regulate  
CC telomerase expression. The method may be used in therapeutic and  
CC prophylactic treatments, diagnostic protocols, research methods and drug  
CC screening procedures, and in particular for treating diseases, trauma and  
CC conditions of the ageing process. The method solves the problem of  
CC shortening of telomeres and the attendant loss of genetic information  
CC from chromosomes during successive cellular divisions.  
XX  
SQ Sequence 8 AA;  
  
Query Match 3.6%; Score 8; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 136 QYSIGGPQ 143  
DB 1 QYSIGGPQ 8  
  
RESULT 12  
ADJ59099  
ID ADJ59099 standard; peptide; 8 AA.  
XX AC  
XX ADJ59099;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Peptide useful for up-regulating telomerase expression.  
XX Telomerase; vulnery.  
XX





DR WPI; 2003-381789/36.  
 DR N-PSDB; ACF64549.  
 XX  
 PT New Proportionbacterium acnes polypeptides and polynucleotides encoding the  
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
 PT or for stimulating an immune response specific for a P. acnes protein.  
 XX  
 XX Example 1; SEQ ID NO 22988; 1481pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
 CC encoding a Proportionbacterium acnes protein. The invention also relates to  
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
 CC immunogenic fragments of P. acnes polypeptides. The invention  
 CC additionally encompasses expression vectors and host cells comprising a  
 CC polynucleotide of the invention; antibodies against polypeptides of the  
 CC invention; fusion proteins comprising a polypeptide of the invention; a  
 CC method for stimulating an immune response specific for a P. acnes  
 CC polypeptide and an isolated T cell population comprising T cells prepared  
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
 CC antigen-presenting cells that express the polypeptide); a method and kit  
 CC for detecting or determining the presence or absence of P. acnes in a  
 CC patient; and a method for inhibiting the development of P. acnes in a  
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
 CC proteins, T cell populations or antigen-presenting cells that express the  
 CC polypeptides are useful for diagnosing, preventing or treating acne  
 CC vulgaris, or for stimulating an immune response specific for a P. acnes  
 CC protein. The polynucleotides can also be used as probes or primers for  
 CC nucleic acid hybridisation. The vaccine composition is useful for the  
 CC stimulation of an immune response against P. acnes, or for treating acne,  
 CC and the kit is useful for performing a diagnostic assay. The present  
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open  
 CC reading frame) contained within the P. acnes polynucleotides of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 235 AA;

Query Match 3.6%; Score 8; DB 6; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 RNSRALLS 68  
 |||||  
 Db 87 RNSRALLS 94

RESULT 15  
 ADD25155  
 ID ADD25155 standard; protein; 598 AA.

XX AC ADD25155;

XX DT 15-JAN-2004 (first entry)

XX DE Fertility restorer protein #15.

XX KW fertility restorer protein; male sterile plant; viable pollen production;  
 KW selection marker.

XX OS Unidentified.

XX PN WO2003006622-A2.

XX PD 23-JAN-2003.

XX PF 12-JUL-2002; 2002WO-US022217.

XX PR 12-JUL-2001; 2001US-0305026P.

XX PR 13-JUL-2001; 2001US-0305363P.

XX PR 30-JUL-2001; 2001US-0308736P.

PA (UYMC-) UNIV MCGILL.  
 PA (DNAL-) DNA LANDMARKS INC.  
 XX  
 PI Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;  
 XX WPI; 2003-221734/21.  
 DR N-PSDB; ADD25156.  
 XX  
 PT New nuclear fertility restorer genes, useful for restoring fertility in  
 PT cytoplasmic male-sterile plants such as Brassica napus plants, or for  
 PT increasing production of viable pollen in a plant.  
 XX  
 PS Claim 5; SEQ ID NO 29; 191pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequences of isolated  
 CC fertility restorer proteins. The DNA and protein sequences of the  
 CC invention are useful for restoring fertility in male sterile plants, such  
 CC as Brassica napus plants. The DNA and protein sequences of the invention  
 CC are useful for increasing production of viable pollen in a plant. The DNA  
 CC and protein sequences are also useful as selection markers to identify  
 CC transformed plant cells. The present amino acid sequence represents a  
 CC fertility restorer protein of the invention.  
 XX  
 SQ Sequence 598 AA;

Query Match 3.6%; Score 8; DB 7; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 74; 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;

QY 201 PSVFTTPS 208  
 |||||  
 Db 332 PSVFTTPS 339

Search completed: June 10, 2006, 03:19:11  
 Job time : 202 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:19:30 ; Search time 40 Seconds  
(without alignments)  
538.814 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 224

Sequence: 1 MPGRAPLRTVPGALGAWLLG.....TPPSTCQMAQLKRWSEDCSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	4.0	1075	1 RNRZB	DNA-directed RNA p
2	7	3.1	130	2 B72702	hypothetical prote
3	7	3.1	158	2 B84268	hypothetical prote
4	7	3.1	167	2 T33602	hypothetical prote
5	7	3.1	194	2 T26391	hypothetical prote
6	7	3.1	243	2 T19090	hypothetical prote
7	7	3.1	253	2 H83238	probable peptidyl-
8	7	3.1	277	2 D98085	hypothetical prote
9	7	3.1	278	2 E95221	sugar ABC transpor
10	7	3.1	297	2 T27584	hypothetical prote
11	7	3.1	353	2 A89933	Xaa-Pro dipeptidas
12	7	3.1	354	2 D86879	ornithine carbamoy
13	7	3.1	368	2 T44305	probable pyruvate
14	7	3.1	369	2 T51477	glutamine-rich pro
15	7	3.1	381	2 T34692	probable transmemb
16	7	3.1	420	2 G95005	phosphoribosylamin
17	7	3.1	420	2 D97878	phosphoribosylamin
18	7	3.1	432	2 T16639	hypothetical prote
19	7	3.1	437	2 C72213	conserved hypothet
20	7	3.1	506	2 T35261	probable metallopro
21	7	3.1	508	2 C95282	probable ABC trans
22	7	3.1	545	2 AC3101	hypothetical prote
23	7	3.1	545	2 G98185	hypothetical prote
24	7	3.1	598	2 B90589	sugar ABC transpor
25	7	3.1	643	2 A97234	ABC-type transport
26	7	3.1	759	2 B83474	probable type II s
27	7	3.1	810	1 DEECK2	metL bifunctional
28	7	3.1	810	2 A86085	aspartokinase II /
29	7	3.1	810	2 E91237	aspartokinase II /

30	7	3.1	811	2 AB0015	aspartate kinase (
31	7	3.1	873	2 E90581	hypothetical prote
32	7	3.1	974	2 T29545	hypothetical prote
33	7	3.1	1070	2 B86922	probable arabinosy
34	7	3.1	1200	2 T15921	hypothetical prote
35	7	3.1	2733	2 S15760	genome polyprotein
36	6	2.7	28	4 JN0014	GABA(A) receptor a
37	6	2.7	46	2 165268	collagen alpha 1(I
38	6	2.7	54	2 B48834	basic fibroblast g
39	6	2.7	78	2 S17872	translation initia
40	6	2.7	81	1 C70910	hypothetical prote
41	6	2.7	95	2 A56842	transcription fact
42	6	2.7	99	2 G70509	hypothetical prote
43	6	2.7	101	2 C72537	hypothetical prote
44	6	2.7	101	2 G71017	hypothetical prote
45	6	2.7	107	2 S63991	thioredoxin trxA -

ALIGNMENTS

RESULT 1

RNRZB

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - rice chloroplast  
C;Species: Chloroplast Oryza sativa (rice)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: JQ0213, S05093  
R;Shimada, H.; Whittier, R.F.; Hiratsuka, J.; Maeda, Y.; Hirai, A.; Sugiyura, M.  
submitted to JIPID, December 1989  
A;Reference number: JQ0200  
A;Accession: JQ0213  
A;Molecule type: DNA  
A;Residues: 1-1075 <SHI>  
A;Cross-references: UNIPROT:P12091; UNIPARC:UPI000001346ED  
A;Experimental source: cv. Nihonbare  
R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kon.

Mol. Gen. Genet. 217, 185-194, 1989  
A;Title: The complete sequence of the rice (Oryza sativa) chloroplast genome: intermol  
of the cereals.  
A;Reference number: S05080; MUID:89364698; PMID:2770692  
A;Accession: S05093  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
A;Residues: 1-1075 <HIR>  
A;Cross-references: UNIPARC:UPI00001346ED; EMBL:X15901; NID:g11957; PIDN:CAA33986.1; P  
A;Experimental source: cv. Nihonbare  
C;Genetics:  
A;Gene: rpoB  
A;Map position: CP19214-22441  
A;Map position: Chloroplast  
A;Genome: Chloroplast  
C;Superfamily: DNA-directed RNA polymerase beta chain  
C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 4.0%; Score 9; DB 1; Length 1075;  
Best Local Similarity 100.0%; Pred. No. 0.83;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 LDIPQNSTF 133  
|||  
Db 270 LDIPQNSTF 278

RESULT 2

B72702

hypothetical protein AP1033 - Aeropyrum pernix (strain K1)  
C;Species: Aeropyrum pernix  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: B72702  
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka  
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;  
DNA Res. 6, 83-101, 1999  
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A;Reference number: A72450; MUID:99310339; PMID:10382966  
A;Accession: B72702  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-130 <KAW>  
A;Cross-references: UNIPROT:Q9YD79; UNIPARC:UPI000005DDAF; DBJ:AP0000060; NID:g5104188;  
A;Experimental source: strain K1  
C;Genetics:  
A;Gene: APE1033

Query Match 3.1%; Score 7; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LCGLCSL 33  
|||||  
Db 100 LCGLCSL 106

RESULT 3  
B84268  
hypothetical protein Vng1120h [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84268  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabcz  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: B84268  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-158 <STO>  
A;Cross-references: UNIPROT:Q9HQK3; UNIPARC:UPI00000637FB; GB:AE004437; NID:g10580662; F  
C;Genetics:  
A;Gene: VNG1120H

Query Match 3.1%; Score 7; DB 2; Length 158;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LGAVGAP 39  
|||||  
Db 131 LGAVGAP 137

RESULT 4  
T33602  
hypothetical protein E02H9.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33602  
R;Kellen, J.; Kramer, J.; Hawkins, M.  
submitted to the EMBL Data Library, October 1998  
A;Description: The sequence of C. elegans cosmid E02H9.  
A;Reference number: Z21375  
A;Accession: T33602  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-167 <REL>  
A;Cross-references: UNIPROT:Q9TZ96; UNIPARC:UPI000017B8A0; EMBL:AF099915; PIDN:AAC68768.  
A;Experimental source: strain Bristol N2; clone E02H9  
C;Genetics:  
A;Gene: CESP:E02H9.2  
A;Map position: 3  
A;Introns: 89/2

Query Match 3.1%; Score 7; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GLCSLGA 35  
|||||  
Db 122 GLCSLGA 128

RESULT 5  
T26391  
hypothetical protein Y105C5B.O - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26391  
R;McMurray, A.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20208  
A;Accession: T26391  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-194 <WIL>  
A;Cross-references: UNIPROT:Q9NAM3; UNIPARC:UPI00001641E1; EMBL:AL110479; PIDN:CAB54363  
A;Experimental source: clone Y105C5B  
C;Genetics:  
A;Gene: CESP:Y105C5B.O  
A;Introns: 13/1; 56/3; 155/2

Query Match 3.1%; Score 7; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LIPCKRL 91  
|||||  
Db 122 LIPCKRL 128

RESULT 6  
T19090  
hypothetical protein C08F11.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19090  
R;Matthews, L.  
submitted to the EMBL Data Library, December 1996  
A;Reference number: Z19072  
A;Accession: T19090  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-243 <WIL>  
A;Cross-references: UNIPROT:O62049; UNIPARC:UPI0000060ECC; EMBL:Z83216; PIDN:CAB05674.1  
A;Experimental source: clone C08F11  
C;Genetics:  
A;Gene: CESP:C08F11.3  
A;Map position: 4  
A;Introns: 14/2; 80/1; 158/2

Query Match 3.1%; Score 7; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 LPEYILL 97  
|||||  
Db 149 LPEYILL 155

RESULT 7  
H83238  
probable peptidyl-prolyl cis-trans isomerase, Fkbp-type PA3262 [imported] - Pseudomonas  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: H83238  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: H83238  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-253 <STO>  
A;Cross-references: UNIPROT:Q9HYX8; UNIPARC:UPI00000C597F; GB:AE004748; GB:AE004091; NID  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3262  
C;Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKEP-type peptidylprolyl isomerase  
Query Match 3.1%; Score 7; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 196 LGIKDPS 202  
Db 225 LGIKDPS 231  
RESULT 8  
D98085  
hypothetical protein msmG [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C;Accession: D98085  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eick, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; J. Bacteriol. 183, 5709-5717, 2001  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: D98085  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-277 <KUR>  
A;Cross-references: UNIPROT:Q8DN10; UNIPARC:UPI00000E36DD; GB:AE007317; PIDN:AAL00513.1;  
C;Genetics:  
A;Gene: msmG  
C;Superfamily: maltose transport protein malG  
Query Match 3.1%; Score 7; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 80 DERKALI 86  
Db 4 DERKALI 10  
RESULT 9  
E95221  
sugar ABC transporter, permease protein SP1895 [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: E95221  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, M.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: E95221  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-278 <KUR>  
A;Cross-references: UNIPROT:Q9TNW4; UNIPARC:UPI00000C9CFA; GB:AE005672; PIDN:AAK75966.1;  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP1895

C;Superfamily: maltose transport protein malG

Query Match 3.1%; Score 7; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 DERKALI 86

Db 5 DERKALI 11

RESULT 10

T27584

hypothetical protein ZC455.9 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T27584

R;Lightning, J.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z20390

A;Accession: T27584

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-297 <WIL>

A;Cross-references: UNIPROT:Q23339; UNIPARC:UPI000007E8AE; EMBL:Z75554; PIDN:CAA99960.1

A;Experimental source: clone ZC455

C;Genetics:

A;Gene: CRSP:ZC455.9

A;Map position: 5

A;Introns: 62/1; 180/3; 211/3; 245/3

Query Match 3.1%; Score 7; DB 2; Length 297;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 ILSTRFF 192

Db 95 ILSTRFF 101

RESULT 11

A89933

Xaa-Pro dipeptidase [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C;Accession: A89933

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: A89933

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-353 <KUR>

A;Cross-references: UNIPROT:Q9TW4; UNIPARC:UPI00000C7F79; GB:BA000018; PID:gl3701328;

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA1360

C;Superfamily: X-Pro aminopeptidase

QY 106 IDQATKQ 112

Db 56 IDQATKQ 62

Query Match 3.1%; Score 7; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

D86879

ornithine carbamoyltransferase (EC 2.1.1.3.3) [imported] - Lactococcus lactis subsp. lactis  
C:Species: Lactococcus lactis subsp. lactis  
C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 31-Dec-2004  
C:Accession: D86879  
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: D86879  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-354 <STO>  
A:Cross-references: UNIPROT:Q9CE14; UNIPARC:UPI00000C6B9A; GB:AE005176; PID:gl2725085; F  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arcB  
C:Superfamily: ornithine/aspartate carbamoyltransferase; aspartate/ornithine carbamoyltr  
C:Keywords: transferase

Query Match 3.1%; Score 7; DB 2; Length 354;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DIQLGIK 199  
|||||  
DB 92 DIQLGIK 98

RESULT 13  
T44305  
probable pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) E1-alpha chain [imported] - Hal  
C:Species: Haloflex volcanii  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T44305  
R:Jolley, K.A.; Maddocks, D.G.; Gyles, S.L.; Sinclair, Z.; Dyal-Smith, M.L.; Hough, D.W  
submitted to the EMBL Data Library, May 1998  
A:Description: 2-Oxoacid dehydrogenase multienzyme complexes in the halophilic Archaea;  
A:Reference number: Z22746  
A:Accession: T44305  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-368 <JOL>  
A:Cross-references: UNIPROT:Q9Y815; UNIPARC:UPI0000062775; EMBL:AF068743; PIDN:AAD34202.  
A:Experimental source: strain WFD11  
C:Genetics:  
A:Gene: pdhA  
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bir  
C:Keywords: oxidoreductase

Query Match 3.1%; Score 7; DB 2; Length 368;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 RVRVLDE 81  
|||||  
DB 11 RVRVLDE 17

RESULT 14  
T51477  
Glutamine-rich protein - Arabidopsis thaliana  
N:Alternate names: protein K3M16\_80  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: T51477  
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew  
submitted to the Protein Sequence Database, August 2000  
A:Reference number: Z25394  
A:Accession: T51477  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-369 <SAT>  
A:Cross-references: UNIPROT:Q9LFS1; UNIPARC:UPI00000A0544; EMBL:ALJ391150

A:Experimental source: cultivar Columbia; BAC clone K3M16  
C:Genetics:  
A:Map position: 5  
A:Introns: 160/2  
A>Note: K3M16\_80

Query Match 3.1%; Score 7; DB 2; Length 369;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 DERKALI 86  
|||||  
DB 243 DERKALI 249

RESULT 15  
T34692  
probable transmembrane transport protein - Streptomyces coelicolor (fragment)  
C:Species: Streptomyces coelicolor  
C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: T34692  
R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, May 1998  
A:Reference number: Z21553  
A:Accession: T34692  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-381 <HAR>  
A:Cross-references: UNIPROT:O8CJP5; UNIPARC:UPI000017AE03; EMBL:AL023517; PIDN:CAA18988  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC1B5.14c

Query Match 3.1%; Score 7; DB 2; Length 381;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RTVPGAL 14  
|||||  
DB 79 RTVPGAL 85

Search completed: June 10, 2006, 03:24:58  
Job time : 43 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 03:15:55 ; Search time 296 Seconds  
(without alignments)  
700.012 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 224

Sequence: 1 MPCRPLRTVPGALGAWLLG.....TPPSTCQMAQLEKWSDECSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224	100.0	224	1 EPDR1_HUMAN	Q9um22 homo sapien
2	206	92.0	344	2 Q96J80_HUMAN	Q96j80 homo sapien
3	103	46.0	224	2 Q99M77_MOUSE	Q99m77 mus musculu
4	85	37.9	224	1 EPDR1_MACFA	Q9n0c7 macaca fasc
5	59	26.3	227	2 Q9SK77_MACFA	Q9sk77 macaca fasc
6	54	24.1	227	2 Q9SK54_MACFA	Q9sk54 macaca fasc
7	39	17.4	224	2 Q5X110_RAT	Q5x110 rattus norv
8	33	14.7	218	2 Q9SK56_MACFA	Q9sk56 macaca fasc
9	32	14.3	224	2 Q8BOY1_MOUSE	Q8bqy1 mus musculu
10	32	14.3	224	2 Q8CAI2_MOUSE	Q8ca12 mus musculu
11	32	14.3	224	2 Q99M71_MOUSE	Q99m71 m mammalian
12	9	4.0	206	2 Q6DH25_BRARE	Q6dh25 brachydanio
13	9	4.0	817	2 Q8DCT9_VIBVU	Q8dct9 vibrio vuln
14	9	4.0	819	2 Q7MH12_VIBVU	Q7mh12 vibrio vuln
15	9	4.0	1067	2 Q6QXV7_ORYSA	Q6qxv7 oryza sativ
16	9	4.0	1067	2 Q7DNA7_ORYSA	Q7dna7 oryza sativ
17	9	4.0	1067	2 Q7XW77_ORYSA	Q7xw77 oryza sativ
18	9	4.0	1075	1 RPOB_ORYNI	Q6en14 oryza nivar
19	9	4.0	1075	1 RPOB_ORYSA	P12091 oryza sativ
20	9	4.0	1075	2 Q6QY83_ORYSA	Q6qy83 oryza sativ
21	9	4.0	1143	2 Q4BOM6_BURVI	Q4bm6 burkholderi
22	9	4.0	1427	2 Q339H4_ORYSA	Q339h4 oryza sativ
23	8	3.6	140	2 Q6IIF2_DROME	Q6iif2 drosophila
24	8	3.6	185	2 Q2N779_9SPHN	Q2n779 erythrobact
25	8	3.6	203	2 Q6WNG6_BRARE	Q6wng6 branchiost
26	8	3.6	223	2 Q8XNU6_CLOPE	Q8xnu6 clostridium
27	8	3.6	308	2 Q7NNL6_GLOVI	Q7nnl6 gloeobacter
28	8	3.6	420	2 Q410H5_KINRA	Q410h5 kinococcus
29	8	3.6	514	2 Q64BG4_9ARCH	Q64bg4 uncultured
30	8	3.6	536	2 Q4CVM0_TRYCR	Q4cvm0 trypanosoma
31	8	3.6	538	2 Q4D988_TRYCR	Q4d988 trypanosoma

32	8	3.6	774	2 Q746U9_GEOSL	Q746u9 geobacter s
33	8	3.6	798	2 Q8SUR3_ENCCU	Q8sur3 encephalito
34	8	3.6	856	2 Q6AAP2_PROAC	Q6aap2 propionibac
35	8	3.6	1198	2 Q3QV23_9RHOB	Q3qv23 silicibacte
36	7	3.1	85	2 Q67JWS_SYMTH	Q67jws symbiobacte
37	7	3.1	88	2 Q6LXM0_METMP	Q6lxm0 methanococc
38	7	3.1	96	2 Q424Y1_DESHA	Q424y1 desulfitoba
39	7	3.1	109	2 Q4UTN8_XANC8	Q4utn8 xanthomonas
40	7	3.1	109	2 Q8P9Z7_XANCP	Q8p9z7 xanthomonas
41	7	3.1	113	2 Q4H7B9_9DEIO	Q4h7b9 deinoxococcus
42	7	3.1	116	2 Q47IP0_DECAR	Q47ip0 dechloromon
43	7	3.1	122	2 Q3MVP8_9DELT	Q3mvp8 syntrophoba
44	7	3.1	130	2 Q9YD79_AERPE	Q9yd79 aeropyrum p
45	7	3.1	130	2 Q8KBE6_CHLTE	Q8keef chlorobium

#### ALIGNMENTS

RESULT 1  
EPDR1\_HUMAN  
ID EPDR1\_HUMAN STANDARD; PRT; 224 AA.  
AC Q9UM22;  
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.  
DT 21-FEB-2001, sequence version 2.  
DT 07-FEB-2006, entry version 40.  
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).  
DE Protein).  
GN Name=EPDR1; Synonyms=MERP1, UCC1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M., Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;  
RT "Identification and characterization of a novel family of mammalian ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic, and malignant tissues."  
RT DNA Cell Biol. 20:625-635 (2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Cervix;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 51-224.  
RA Nimrich I., Erdmann S., Melchers U.;  
RT "Genes that are differentially expressed in colon cancer."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Secreted protein.





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CC -----  
DR EMBL; AY027861; AAK15787.1; -; mRNA.  
DR MGI; MGI-2152290; Epdrl.  
DR MGI; MGI-2152290; Ucc1.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.  
DR InterPro; IPR001299; Ependymin.  
DR PANTHER; PTHR10697; Ependymin; 1.  
DR PRINTS; PR00317; EPENDYMIN.  
DR ProDom; PD06315; Ependymin; 1.  
DR PROSITE; PS00898; EPENDYMIN\_1; UNKNOWN\_1.  
DR PROSITE; PS00899; EPENDYMIN\_2; 1.  
SQ SEQUENCE 224 AA; 25437 MW; DB6CA5A9A7289E95 CRC64;  
  
Query Match 46.0%; Score 103; DB 2; Length 224;  
Best Local Similarity 99.5%; Pred. No. 4.8e-99;  
Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 21 GLAWTLGCLGSLGAVGAPPCQAPQWEGRGVYQSSGRNSRALLSYDGLNQRVRLD 80  
DB 21 GLAWTLGCLGSLGAVGAPPCQAPQWEGRGVYQSSGRNSRALLSYDGLNQRVRLD 80  
  
QY 81 ERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIG 140  
DB 81 ERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIG 140  
  
QY 141 GPQEQITVQWSRKSARSYETWIGIYTVKDCYPVQSTFTINYSVILSTRFFDIQLGIKD 200  
DB 141 GPQEQITVQWSRKSARSYETWIGIYTVKDCYPVQSTFTINYSVILSTRFFDIQLGIKD 200  
  
QY 201 PSVFTPPSTCQMAQLKMSDCSW 224  
DB 201 PSVFTPPSTCQMAQLKMSDCSW 224  
  
RESULT 4  
EPDR1 MACFA  
ID EPDR1 MACFA STANDARD; PRT; 224 AA.  
AC Q9NOC7;  
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.  
DT 21-FEB-2006, entry version 2.  
DT 07-FEB-2006, entry version 31.  
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).  
GN Name=EPDR1; Synonyms=MERP1, UCC1; ORFNames=QcCE-12983;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC Tissue=Brain cortex;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Secreted protein.  
CC -!- SIMILARITY: Belongs to the ependymin family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AB046003; BAB01585.1; ALT\_INIT; mRNA.  
DR LinkHub; Q9NOC7; -;  
DR InterPro; IPR001299; Ependymin.  
DR PANTHER; PTHR10697; Ependymin; 1.  
DR PRINTS; PR00317; EPENDYMIN.  
DR ProDom; PD06315; Ependymin; 1.  
DR PROSITE; PS00898; EPENDYMIN\_1; 1.  
KW Hypothetical protein.

DR PROSITE; PS00899; EPENDYMIN\_2; 1.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 37 Potential.  
FT CHAIN 38 224 Mammalian ependymin-related protein 1.  
FT CARBOHYD 130 130 /FTID=PRO\_000008352.  
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 224 AA; 25484 MW; 3594311D15AB4BB7 CRC64;  
  
Query Match 37.9%; Score 85; DB 1; Length 224;  
Best Local Similarity 100.0%; Pred. No. 3.8e-80;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 22 LWAWTLGCLGSLGAVGAPPCQAPQWEGRGVYQSSGRNSRALLSYDGLNQRVRLD 81  
DB 22 LWAWTLGCLGSLGAVGAPPCQAPQWEGRGVYQSSGRNSRALLSYDGLNQRVRLD 81  
  
QY 82 RKALIPCKRLFEVILLYKDGVMFQI 106  
DB 82 RKALIPCKRLFEVILLYKDGVMFQI 106  
  
RESULT 5  
Q95K77 MACFA  
ID Q95K77 MACFA PRELIMINARY; PRT; 227 AA.  
AC Q95K77;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Temporal lobe right;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Medulla oblongata;  
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes";  
RL Gene 275:31-37(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Medulla oblongata;  
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AB063094; BAB060800.1; -; mRNA.  
DR EMBL; AB097520; BAC41745.1; -; mRNA.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.  
DR InterPro; IPR001299; Ependymin.  
DR PANTHER; PTHR10697; Ependymin; 1.  
DR PRINTS; PR00317; EPENDYMIN.  
DR ProDom; PD06315; Ependymin; 1.  
DR PROSITE; PS00898; EPENDYMIN\_1; UNKNOWN\_1.  
DR PROSITE; PS00899; EPENDYMIN\_2; 1.  
KW Hypothetical protein.

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Musny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RX NIH MGC Project;

RG Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL; BC083701.1; AAH83701.1; -; mRNA.

DR Ensembl; ENSRNOG0000018989; Rattus norvegicus.

DR GO; GO:005576; C:extracellular region; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0007160; P:cell-matrix adhesion; IEA.

DR InterPro; IPR001299; Ependymin.

DR PANTHER; PTHR10697; Ependymin; 1.

DR PRINTS; PR00317; EPENDYMIN.

DR ProDom; PD006315; Ependymin; 1.

DR SEQUENCE 224 AA; 25639 MW; B8DE78133B1CCB21 CRC64;

SQ

Query Match 17.4%; Score 39; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 7,1e-32;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVLDERKALIPCKRLFEYILLYKDGVMFQI 106

DB 68 SYDGLNQRVLDERKALIPCKRLFEYILLYKDGVMFQI 106

|||||

RESULT 8

Q95K56 MACFA PRELIMINARY; PRT; 218 AA.

ID ID Q95K56 MACFA PRELIMINARY; PRT; 218 AA.

AC Q95K56;

DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecidae; Cercopitheciinae; Macaca.

OC NCBI\_Taxid=9541;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RP TISSUE=Medulla oblongata;

RC Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;

RT "Isolation of full-length cDNA clones from macaque brain cDNA

RT libraries.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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CC -----
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CC -----
DR ENBL; AB066535; BAB2211.1; -, mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin.
DR PRINTS; PR00317; Ependymin.
DR PRODOM; PD006315; Ependymin.
DR PROSITE; PS00898; Ependymin_1.
DR PROSITE; PS00899; Ependymin_2; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 218 AA; 24970 MW; 8B8524C0D986677C CRC64;

Query Match 14.7%; Score 33; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 VQWSDRKSARSYETWIGTVKDCYPVQSTFT 180
Db 142 VQWSDRKSARSYETWIGTVKDCYPVQSTFT 174

RESULT 9
Q8BOY1_MOUSE PRELIMINARY; PRT; 224 AA.
AC Q8BOY1;
DT 01-MAR-2003, integrated into UniprotKB/TREMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
DE library, clone:B230347119 product:MAMMALIAN EPENDYMIN RELATED PROTEIN-
DE 2 (SIMILAR TO MAMMALIAN EPENDYMIN RELATED PROTEIN 1) homolog.
GN Names=Epd12; Synonyms=AU040950;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Katayama T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashiki Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lacroix L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Mader M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
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RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Aragawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira T.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Ruelh P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaado I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Wacker D., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaado I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;

RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,

RA Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [8]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL; AK038733; BAC30113.1; -; mRNA.

DR Ensembl; ENSMUSG00000002808; Mus musculus.

DR MGI; MGI:2145369; AU040950.

DR MGI; MGI:2145369; Eppd2.

DR GO; GO:0005615; C:extracellular space; RCA.

DR GO; GO:0005509; F:calcium ion binding; RCA.

DR GO; GO:0007160; P:cell-matrix adhesion; RCA.

DR InterPro; IPR001299; Ependymin.

DR PANTHER; PTHR10697; Ependymin; 1.

DR PRINTS; PR00317; Ependymin.

DR PRODOM; PD006315; Ependymin; 1.

SQ SEQUENCE 224 AA; 25515 MW; D49BAC6C8A4857BB CRC64;

Query Match 14.3%; Score 32; DB 2; Length 224;

Best Local Similarity 100.0%; Pred.No. 1.6e-24;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 SYDGLNQVRVLDERKALIFCKLFEYLLYK 99

Db 68 SYDGLNQVRVLDERKALIFCKLFEYLLYK 99

|||||

RESULT 11

Q99M71\_MOUSE PRELIMINARY; PRT; 224 AA.

ID Q99M71\_MOUSE

AC Q99M71;

DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 29.

DE Mammalian ependymin related protein-2 (Ependymin 2) (Adult male

DE diencephalon cDNA, RIKEN full-length enriched library,

DE clone:9330154O03 product:mammalian ependymin related protein-2

DE male cerebellum cDNA, RIKEN full-length enriched library,

DE clone:1500034M21 product:Mammalian ependymin related protein-2

DE (similar to mammalian ependymin related protein 1), full insert

DE sequence).

GN Name=Eppd2; Synonyms=AU040950, MERP2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN NUCLEOTIDE SEQUENCE.

STRAIN=C57BL6/J, and C57BL/6J;  
MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;  
Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,  
Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;  
"Identification and characterization of a novel family of mammalian  
ependymin-related proteins (NERPs) in hematopoietic, nonhematopoietic,  
and malignant tissues.";  
DNA Cell Biol. 20:625-635 (2001).  
[2]

NUCLEOTIDE SEQUENCE.

STRAIN=FVB/N; TISSUE=Kidney;  
MEDLINE=223828257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[3]

NUCLEOTIDE SEQUENCE.

STRAIN=FVB/N; TISSUE=Kidney;  
Director MGC Project;  
Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.  
[4]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
Carninci P., Hayashizaki Y.;  
"High-efficiency full-length cDNA cloning";  
Methods Enzymol. 303:19-44 (1999).  
[5]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
PubMed=16141072; DOI=10.1126/science.1112014;  
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,  
Ajima R.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,  
Ambesi-Impombato A., Ansel K.W., Bersano T., Bailey T.L.,  
Banerl M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
Hill D., Humnick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,  
Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
Mottagui-Far S., Mulder N., Nakano N., Nakachi H., Ng P.,  
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L.,  
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sheng Y.,

Sperling S., Stupka E., Sugiyura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verdaro R., Wei C.B., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.,  
"The transcriptional landscape of the mammalian genome.",  
Science 309:1559-1563 (2005).  
[6]  
Nucleotide Sequence.  
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
PubMed=16141073; DOI=10.1126/science.1112009;  
RIKEN Genome Exploration Research Group, and Genome Science Group  
(Genome Network Core Team) and the FANTOM Consortium;  
"Antisense Transcription in the Mammalian Transcriptome";  
Science 309:1564-1566 (2005).  
[7]  
Nucleotide Sequence.  
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konogaya A., Kurochkin I.V., Lee Y., Lennhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertele G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verdaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kigawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;  
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
Nature 420:563-573 (2002).  
[8]  
Nucleotide Sequence.  
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
MEDLINE=21085660; PubMed=11217951; DOI=10.1038/35055500;  
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto T.,



RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Yashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [9]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [10]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitaunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [11]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
Query Match 14.3%; Score 32; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. NO. 1.6e-24;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQRVRLDKALIPCKLFVYLLYK 99  
DB 68 SYDGLNQRVRLDKALIPCKLFVYLLYK 99  
RESULT 12  
Q6DH25\_BRARE PRELIMINARY; PRT; 206 AA.  
AC Q6DH25;  
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
DT 16-AUG-2004, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Ependymin related protein 1.  
GN Name=epdri;  
OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Eye;  
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Eye;  
RG NIH MGC Project;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BC076158; AAH76158.1; -; mRNA.  
DR Ensembl; ENSDARG0000045420; Danio rerio.  
DR ZFIN; ZDB-GENE-040718-113; epdri.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.  
DR InterPro; IPR0010697; Ependymin.  
DR PANTHER; PTHR10697; Ependymin; 1.  
DR PRINTS; PR00317; Ependymin.  
DR ProDom; PD006315; Ependymin; 1.  
SQ SEQUENCE 206 AA; 23467 MW; 64646DEB4506530D CRC64;  
Query Match 4.0%; Score 9; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. NO. 2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 170 KDCYPVQET 178  
DB 154 KDCYPVQET 162  
RESULT 13  
Q8DCT9\_VIBVU PRELIMINARY; PRT; 817 AA.  
AC Q8DCT9;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE Exoribonuclease R.  
GN OrderedLocNames=VV11304; ORFNames=VV1\_1304;  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=672;  
RN [1]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AE016795; AAC09759.1; -; Genomic\_DNA.  
DR BioCyc; VVU1216895:VV11304-MONOMER; -.  
DR GO; GO:0004540; F:ribonuclease activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0016070; P:RNA metabolism; IEA.  
DR InterPro; IPR011129; CSP.  
DR InterPro; IPR012340; OB\_NA\_bd\_sub.  
DR InterPro; IPR013223; RNase\_B\_OB\_N.  
DR InterPro; IPR001900; RNase\_II\_R.  
DR InterPro; IPR004476; RNase\_II\_R\_bac.

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DR InterPro; IPR011805; RNase R bac.
DR InterPro; IPR003029; Sl_RNA_Ed.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00773; RNB; 2.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMs; TIGR00358; 3_prime_RNase; 1.
DR TIGRFAMs; TIGR02063; RNase R; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
DR PROSITE; PS0126; S1; 1.
KW Complete proteome.
SQ SEQUENCE 817 AA; 93124 MW; F33DB28163DDAF83 CRC64;

Query Match 4.0%; Score 9; DB 2; Length 817;
Best Local Similarity 100.0%; Pred.No.6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VRVLDERKA 84
DB 149 VRVLDERKA 157

RESULT 14
Q7MH12_VIBVY PRELIMINARY; PRT; 819 AA.
AC Q7MH12;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Exoribonuclease R.
GN OrderedLocName=V3061;
OS Vibrio vulnificus (strain Y0016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
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-----
DR EMBL; BA000037; BAC95925.1; -; Genomic_DNA.
DR BioCyc; VVUL196600:V3061-MONOMER; -.
DR GO; GO:0004540; F:ribonuclease activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016070; P:RNA metabolism; IEA.
DR InterPro; IPR011129; CSP.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR013223; RNase_B_OB_N.
DR InterPro; IPR001900; RNase_II_R.
DR InterPro; IPR004476; RNase_II_R_bac.
DR InterPro; IPR011805; RNase_R_bac.
DR InterPro; IPR003029; Sl_RNA_Ed.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00773; RNB; 2.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMs; TIGR00358; 3_prime_RNase; 1.
DR TIGRFAMs; TIGR02063; RNase R; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
DR PROSITE; PS0126; S1; 1.
KW Complete proteome.
SQ SEQUENCE 819 AA; 93342 MW; D52BE95D603D4D26 CRC64;

Query Match 4.0%; Score 9; DB 2; Length 1067;
Best Local Similarity 100.0%; Pred.No.8.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 LDIPQNSTF 133
DB 262 LDIPQNSTF 270

Search completed: June 10, 2006, 03:24:12
Job time : 300 secs

Query Match 4.0%; Score 9; DB 2; Length 819;
Best Local Similarity 100.0%; Pred.No.6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VRVLDERKA 84
DB 151 VRVLDERKA 159

RESULT 15
Q6QXV7_ORYSA PRELIMINARY; PRT; 1067 AA.
AC Q6QXV7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE RNA polymerase beta chain.
GN Name=rpoB; ORFNames=Nip036, PA036;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP PubMed=15122023; DOI=10.1104/pp.103.031245;
RA Tang J., Xia H., Cao M., Zhang X., Zeng W., Hu S., Tong W., Wang J.,
RA Wang J., Yu J., Yang H., Zhu L.;
RT "A Comparison of Rice Chloroplast Genomes.";
RL Plant Physiol. 135:412-420(2004).
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-----
DR EMBL; AY522331; AAS46174.1; -; Genomic_DNA.
DR EMBL; AY522330; AAS46111.1; -; Genomic_DNA.
DR Gramene; Q6QXV7; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007121; RNA_pol_B.
DR InterPro; IPR007644; RNA_pol_Rpb2_1.
DR InterPro; IPR007642; RNA_pol_Rpb2_2.
DR InterPro; IPR007645; RNA_pol_Rpb2_3.
DR InterPro; IPR007120; RNA_pol_Rpb2_6.
DR InterPro; IPR007641; RNA_pol_Rpb2_7.
DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
SQ SEQUENCE 1067 AA; 120770 MW; F643A6F524D7CD38 CRC64;

Query Match 4.0%; Score 9; DB 2; Length 1067;
Best Local Similarity 100.0%; Pred.No.8.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 LDIPQNSTF 133
DB 262 LDIPQNSTF 270

Search completed: June 10, 2006, 03:24:12
Job time : 300 secs
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:24:26 ; Search time 50 Seconds  
(without alignments)  
392.137 Million cell updates/sec

**Title:** US-10-733-646-2

Perfect score: 224  
Sequence: 1 MPGRAPLRTVPALGAWLLG.....TPPSTCOMAQLEKMSSEDCSW 224

Scoring table: OLIGO

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649247

Minimum DB seq length: 0

Maximum DB seq length: 200000000

### Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \*

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2: /EMC Celerra SID33 /tcdatata/2/iaa/6 COMB pep.*
3: /EMC Celerra SID33 /tcdatata/2/iaa/7 COMB pep.*
4: /EMC Celerra SID33 /tcdatata/2/iaa/8 COMB pep.*
5: /EMC Celerra SID33 /tcdatata/2/iaa/9 PCTUS COMB pep.*
6: /EMC Celerra SID33 /tcdatata/2/iaa/RE COMB pep.*
7: /EMC Celerra SID33 /tcdatata/2/iaa/backfiles pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	224	100.0	224	2	US-09-229-583A-2	Sequence 2, Appli
2	224	100.0	224	2	US-09-242-890-11	Sequence 11, Appli
3	224	100.0	224	2	US-10-187-904-2	Sequence 2, Appli
4	200	89.3	200	2	US-09-242-890-10	Sequence 10, Appli
5	187	83.5	187	2	US-09-242-890-1	Sequence 1, Appli
6	39	17.4	39	2	US-09-242-890-8	Sequence 8, Appli
7	39	17.4	190	2	US-09-242-890-2	Sequence 2, Appli
8	39	17.4	224	2	US-09-242-890-12	Sequence 12, Appli
9	37	16.5	37	2	US-09-242-890-14	Sequence 14, Appli
10	32	14.3	32	2	US-09-242-890-5	Sequence 5, Appli
11	32	14.3	187	2	US-09-242-890-3	Sequence 3, Appli
12	32	14.3	224	2	US-09-242-890-13	Sequence 13, Appli
13	26	11.6	26	2	US-09-242-890-9	Sequence 9, Appli
14	25	11.2	25	2	US-09-242-890-6	Sequence 6, Appli
15	24	10.7	24	2	US-09-242-890-15	Sequence 15, Appli
16	17	7.6	17	2	US-09-242-890-7	Sequence 7, Appli
17	13	5.8	13	2	US-09-242-890-4	Sequence 4, Appli
18	8	3.6	8	2	US-09-715-763A-12	Sequence 12, Appli
19	8	3.6	8	2	US-09-715-763A-14	Sequence 14, Appli
20	7	3.1	34	2	US-09-242-890-16	Sequence 16, Appli
21	7	3.1	89	2	US-09-252-991A-23279	Sequence 23279, A
22	7	3.1	142	2	US-09-107-433-5033	Sequence 5033, Ap
23	7	3.1	158	2	US-09-496-1188-9	Sequence 9, Appli
24	7	3.1	196	2	US-09-902-540-12288	Sequence 12288, A
25	7	3.1	208	2	US-09-027-287-39	Sequence 39, Appli
26	7	3.1	208	2	US-09-252-6568-39	Sequence 39, Appli

27	7	3.1	208	2	US-09-523-323-39	Sequence 39, Appl
28	7	3.1	213	2	US-09-673-395A-613	Sequence 613, App
29	7	3.1	221	2	US-09-904-615-155	Sequence 155, App
30	7	3.1	221	2	US-10-054-988-155	Sequence 155, App
31	7	3.1	234	2	US-09-252-991A-28420	Sequence 28420, App
32	7	3.1	240	2	US-08-913-014A-1	Sequence 1, Appli
33	7	3.1	240	2	US-09-072-993C-4	Sequence 4, Appli
34	7	3.1	240	2	US-09-072-987-2	Sequence 2, Appli
35	7	3.1	240	2	US-09-252-656B-2	Sequence 2, Appli
36	7	3.1	240	2	US-09-653-285-1	Sequence 1, Appli
37	7	3.1	240	2	US-09-523-323-2	Sequence 2, Appli
38	7	3.1	265	2	US-09-248-796A-16392	Sequence 16392, A
39	7	3.1	277	2	US-09-583-110-2944	Sequence 2944, Ap
40	7	3.1	278	2	US-09-769-787-19	Sequence 19, Appl
41	7	3.1	290	2	US-09-107-433-4262	Sequence 4262, Ap
42	7	3.1	323	2	US-09-252-991A-17899	Sequence 17899, A
43	7	3.1	366	1	US-08-700-359-22	Sequence 22, Appl
44	7	3.1	398	2	US-09-328-352-6411	Sequence 6411, Ap
45	7	3.1	420	2	US-09-583-110-5043	Sequence 5043, Ap

## ALIGNMENTS

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RESULT 1
US-09-229-583A-2
/ Sequence 2, Application US/09229583A
/ Patent No. 6489138
/ GENERAL INFORMATION:
/ APPLICANT: Ebner et al.
/ TITLE OF INVENTION: Human Ependymin
/ FILE REFERENCE: PF403
/ CURRENT APPLICATION NUMBER: US/09/229,583A
/ CURRENT FILING DATE: 1999-01-13
/ PRIOR APPLICATION NUMBER: US 60/071,330
/ PRIOR FILING DATE: 1998-01-14
/ PRIOR APPLICATION NUMBER: US 60/075,278
/ PRIOR FILING DATE: 1998-02-19
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 224
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-229-583A-2

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[illegible]

RESULT 2  
US-09-242-890-11  
; Sequence 11, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasehiro

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/ APPLICANT: Onda, Haruo
/ TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
/ FILE REFERENCE: 2417USOP
/ CURRENT APPLICATION NUMBER: US/09/242,890
/ CURRENT FILING DATE: 1999-02-28
/ PRIOR FILING DATE: 1997-08-10
/ PRIOR APPLICATION NUMBER: PCT/JP97/03194
/ PRIOR FILING DATE: 1996-09-11
/ PRIOR APPLICATION NUMBER: JP 8-240880
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: JP 9-135633
/ PRIOR FILING DATE: 1997-05-27
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE:
/ SEQ ID NO 11
/ LENGTH: 224
/ TYPE: PRT
/ ORGANISM: Human
US-09-242-890-11

Query Match 100.0%; Score 224; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e-220;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFOIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFOIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
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RESULT 3
US-10-187-904-2
/ Sequence 2, Application US/10187904
/ Patent No. 6683161
/ GENERAL INFORMATION:
/ APPLICANT: Ebner et al.
/ TITLE OF INVENTION: Human Ependymin
/ FILE REFERENCE: PF403D1
/ CURRENT APPLICATION NUMBER: US/10/187,904
/ CURRENT FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: US 09/229,583
/ PRIOR FILING DATE: 1999-01-13
/ PRIOR APPLICATION NUMBER: US 60/071,330
/ PRIOR FILING DATE: 1998-01-14
/ PRIOR APPLICATION NUMBER: US 60/075,278
/ PRIOR FILING DATE: 1998-02-19
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 224
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-187-904-2

Query Match 100.0%; Score 224; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e-220;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
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QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFOIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFOIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224

RESULT 4
US-09-242-890-10
/ Sequence 10, Application US/09242890
/ Patent No. 6613887
/ GENERAL INFORMATION:
/ APPLICANT: Ogi, Kasuhiro
/ TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
/ FILE REFERENCE: 2417USOP
/ CURRENT APPLICATION NUMBER: US/09/242,890
/ CURRENT FILING DATE: 1999-02-28
/ PRIOR APPLICATION NUMBER: PCT/JP97/03194
/ PRIOR FILING DATE: 1997-08-10
/ PRIOR APPLICATION NUMBER: JP 8-240880
/ PRIOR FILING DATE: 1996-09-11
/ PRIOR APPLICATION NUMBER: JP 8-318049
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: JP 9-135633
/ PRIOR FILING DATE: 1997-05-27
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE:
/ SEQ ID NO 10
/ LENGTH: 200
/ TYPE: PRT
/ ORGANISM: Human
US-09-242-890-10

Query Match 89.3%; Score 200; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.3e-196;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNLRALLSYDGLNQRVRLDERKA 84
DB 1 WTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNLRALLSYDGLNQRVRLDERKA 60
QY 85 LIPCKRLFEYILLYKDGVMFOIDQATKQCSKMTLTQPDPLDIPONSTFEDQYSIGGPQE 144
DB 61 LIPCKRLFEYILLYKDGVMFOIDQATKQCSKMTLTQPDPLDIPONSTFEDQYSIGGPQE 120
QY 145 QITVQWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPV 204
DB 121 QITVQWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPV 180
QY 205 TFPSTCQMAQLEKMSDCSW 224
DB 181 TFPSTCQMAQLEKMSDCSW 200

RESULT 5
US-09-242-890-1
/ Sequence 1, Application US/09242890
/ Patent No. 6613887
/ GENERAL INFORMATION:
/ APPLICANT: Ogi, Kasuhiro
/ TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
/ FILE REFERENCE: 2417USOP
/ CURRENT APPLICATION NUMBER: US/09/242,890
/ CURRENT FILING DATE: 1999-02-28
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; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-1

Query Match      83.5%; Score 187; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 7.6e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 APPCPAQWEGQWYQSSGRNRRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97
Db 1 APPCPAQWEGQWYQSSGRNRRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60

QY 98 YKDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGPQEQITVQWSDRKS 157
Db 61 YKDGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGPQEQITVQWSDRKS 120

QY 158 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVTPSTCMAQLEK 217
Db 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVTPSTCMAQLEK 180

QY 218 MSDDCSW 224
Db 181 MSDDCSW 187

RESULT 6
US-09-242-890-8
; Sequence 8, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like P
US-09-242-890-8

Query Match      17.4%; Score 39; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
Db 1 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 39
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RESULT 7
US-09-242-890-2
; Sequence 2, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-2

Query Match      17.4%; Score 39; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
Db 34 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 72

RESULT 8
US-09-242-890-12
; Sequence 12, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 12
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-12

Query Match      17.4%; Score 39; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
Db 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
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RESULT 9  
US-09-242-890-14  
; Sequence 14, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; APPLICANT: Onda, Haruo  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 14  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Human  
US-09-242-890-14

Query Match 16.5%; Score 37; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2.6e-30;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVG 37  
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVG 37

RESULT 10  
US-09-242-890-5  
; Sequence 5, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; APPLICANT: Onda, Haruo  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse ependymin  
US-09-242-890-5

Query Match 14.3%; Score 32; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.8e-25;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 105 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 136  
Db 1 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 32

RESULT 11  
US-09-242-890-3  
; Sequence 3, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; APPLICANT: Onda, Haruo  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 3  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-242-890-3

Query Match 14.3%; Score 32; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.5e-24;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 99  
Db 31 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 62

RESULT 12  
US-09-242-890-13  
; Sequence 13, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; APPLICANT: Onda, Haruo  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 13  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-242-890-13

Query Match 14.3%; Score 32; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 1.8e-24;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 99  
Db 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 99

RESULT 13  
US-09-242-890-9  
; Sequence 9, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 9  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like P  
US-09-242-890-9

Query Match 11.6%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.1e-19; Indels 0; Gaps 0;  
Matches 26; Conservative 0; Mismatches 0;  
Qy 121 PWDPLDIPQNSTFEDQYSIGGPQEQI 146  
Db 1 PWDPLDIPQNSTFEDQYSIGGPQEQI 26

RESULT 14  
US-09-242-890-6  
; Sequence 6, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 6  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse  
; OTHER INFORMATION: ependymin-like protein  
US-09-242-890-6

Query Match 11.2%; Score 25; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.2e-18; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;

Qy 159 SYETWIGIYTVKDCYPVQETFTINY 183  
Db 1 SYETWIGIYTVKDCYPVQETFTINY 25  
RESULT 15  
US-09-242-890-15  
; Sequence 15, Application US/09242890  
; Patent No. 6613887  
; GENERAL INFORMATION:  
; APPLICANT: Ogi, Kasuhiro  
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE  
; FILE REFERENCE: 2417USOP  
; CURRENT APPLICATION NUMBER: US/09/242,890  
; CURRENT FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-08-10  
; PRIOR APPLICATION NUMBER: JP 8-240880  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: JP 8-318049  
; PRIOR FILING DATE: 1996-11-28  
; PRIOR APPLICATION NUMBER: JP 9-135633  
; PRIOR FILING DATE: 1997-05-27  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE:  
; SEQ ID NO 15  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Human  
US-09-242-890-15

Query Match 10.7%; Score 24; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.2e-17; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0;  
Qy 1 MPCRAPLRTVPGALGAWLLGGLWA 24  
Db 1 MPCRAPLRTVPGALGAWLLGGLWA 24

Search completed: June 10, 2006, 03:25:51  
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:26:06 ; Search time 16 Seconds  
(without alignments)  
177.005 Million cell updates/sec

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Perfect score: 224  
Sequence: 1 MFCRAPLRTVPGALWLLG.....TPPSTCQMAQLEKMSDCSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 64916 seqs, 12643201 residues

Word size : 1

Total number of hits satisfying chosen parameters: 64889

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 7: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	3.1	365	6	US-10-471-571A-558 Sequence 558, App
2	7	3.1	1866	6	US-10-511-937-2968 Sequence 2968, App
3	6	2.7	39	6	US-10-953-349-25806 Sequence 25806, A
4	6	2.7	118	6	US-10-370-959-111 Sequence 111, App
5	6	2.7	166	6	US-10-953-349-16478 Sequence 16478, A
6	6	2.7	166	6	US-10-953-349-19213 Sequence 19213, A
7	6	2.7	166	6	US-10-953-349-20109 Sequence 20109, A
8	6	2.7	166	6	US-10-953-349-23529 Sequence 23529, A
9	6	2.7	188	6	US-10-953-349-34495 Sequence 34495, A
10	6	2.7	201	6	US-10-953-349-31844 Sequence 31844, A
11	6	2.7	209	6	US-10-370-959-110 Sequence 110, App
12	6	2.7	231	6	US-10-471-571A-1786 Sequence 1786, App
13	6	2.7	238	6	US-10-953-349-31180 Sequence 31180, A
14	6	2.7	255	6	US-10-953-349-38691 Sequence 38691, A
15	6	2.7	256	6	US-10-953-349-1546 Sequence 1546, App
16	6	2.7	259	6	US-10-953-349-16938 Sequence 16938, A
17	6	2.7	262	7	US-11-293-697-4404 Sequence 4404, App
18	6	2.7	270	6	US-10-471-571A-2976 Sequence 2976, App
19	6	2.7	276	6	US-10-953-349-16477 Sequence 16477, A
20	6	2.7	276	6	US-10-953-349-19212 Sequence 19212, A
21	6	2.7	276	6	US-10-953-349-20108 Sequence 20108, A
22	6	2.7	276	6	US-10-953-349-23528 Sequence 23528, A
23	6	2.7	289	6	US-10-953-349-16937 Sequence 16937, A
24	6	2.7	300	7	US-11-264-737-101 Sequence 101, App
25	6	2.7	300	7	US-11-264-737-103 Sequence 103, App

ALIGNMENTS

RESULT 1

US-10-471-571A-558  
; Sequence 558, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026927WO  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWin99, version 1.03  
; SEQ ID NO 558  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(365)  
; OTHER INFORMATION: Xaa-Pro dipeptidase  
US-10-471-571A-558

Query Match 3.1%; Score 7; DB 6; Length 365;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 IDQATKQ 112  
|||  
Db 68 IDQATKQ 74

RESULT 2

US-10-511-937-2968  
; Sequence 2968, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; AND MONITORING TRANSPLANT REJECTION

Sequence 18508, A  
Sequence 26321, A  
Sequence 38690, A  
Sequence 13557, A  
Sequence 365, App  
Sequence 366, App  
Sequence 18507, A  
Sequence 26320, A  
Sequence 38689, A  
Sequence 13556, A  
Sequence 28936, A  
Sequence 1852, App  
Sequence 28935, A  
Sequence 3698, A  
Sequence 31887, A  
Sequence 26319, A  
Sequence 15764, A  
Sequence 18936, A  
Sequence 15763, A  
Sequence 21326, A

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; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2968
; LENGTH: 1866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2968

Query Match          3.1%; Score 7; DB 6; Length 1866;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 ALGAWLL 19
        |||||
Db      1810 ALGAWLL 1816

RESULT 3
US-10-953-349-25806
; Sequence 25806, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25806
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-25806

Query Match          2.7%; Score 6; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      206 PPSTCQ 211
        |||||
Db      32 PPSTCQ 37

RESULT 4
US-10-370-959-111
; Sequence 111, Application US/10370959
; Publication No. US2006008907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170NNIM
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; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-111

Query Match          2.7%; Score 6; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      82 RXALIP 87
        |||||
Db      111 RXALIP 116

RESULT 5
US-10-953-349-16478
; Sequence 16478, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16478
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16478

Query Match          2.7%; Score 6; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
        |||||
Db       2 LGAVGA 7

RESULT 6
US-10-953-349-19213
; Sequence 19213, Application US/10953349
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19213
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19213

Query Match      2.7%; Score 6; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
Db      2 LGAVGA 7

RESULT 7
US-10-953-349-20109
; Sequence 20109, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20109
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20109

Query Match      2.7%; Score 6; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
Db      2 LGAVGA 7

RESULT 8
US-10-953-349-23529
; Sequence 23529, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23529
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23529

Query Match      2.7%; Score 6; DB 6; Length 166;
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34495
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34495

Query Match      2.7%; Score 6; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 LCGLCS 32
Db      36 LCGLCS 41

RESULT 10
US-10-953-349-31844
; Sequence 31844, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31844
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31844

Query Match      2.7%; Score 6; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GRAPLR 8
Db      91 GRAPLR 96

RESULT 11
US-10-370-959-110
; Sequence 110, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
```

```
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170NNIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-110

Query Match      2.7%; Score 6; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      82 RKALIP 87
Db      201 RKALIP 206

RESULT 12
US-10-471-571A-1786
; Sequence 1786, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P02692WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1786
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(231)
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; OTHER INFORMATION: exotoxin 8 [Staphylococcus
US-10-471-571A-1786

Query Match      2.7%; Score 6; DB 6; Length 231;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      136 QYSIGG 141
Db      114 QYSIGG 119

RESULT 13
US-10-953-349-31180
; Sequence 31180, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31180
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31180

Query Match      2.7%; Score 6; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GRAPLR 8
Db      145 GRAPLR 150

RESULT 14
US-10-953-349-38691
; Sequence 38691, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38691
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38691

Query Match      2.7%; Score 6; DB 6; Length 255;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      65 ALLSYD 70
Db      95 ALLSYD 100

RESULT 15
US-10-953-349-1546
; Sequence 1546, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1546  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-1546

Query Match 2.7%; Score 6; DB 6; Length 256;  
Best Local Similarity 100.0%; Pred.No. 70;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 LYKDG 102  
Db 127 LYKDG 132

Search completed: June 10, 2006, 03:29:24  
Job time : 17 secs

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## OM protein - protein search, using sw model

Run on: June 10, 2006, 03:25:10 ; Search time 184 Seconds  
(without alignments)  
563.914 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 224

Sequence: 1 MPCRPLRTVPGALGAWLLG.....TPPSTCQMALEKMSDCSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096103

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC Celerra\_SID33/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /EMC Celerra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 3: /EMC Celerra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pcp.\*
- 4: /EMC Celerra\_SID33/ptodata/2/pubpaa/US10\_PUBCOMB.pcp.\*
- 5: /EMC Celerra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 6: /EMC Celerra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	224	100.0	224	4	US-10-612-788-11
2	224	100.0	224	4	US-10-733-646-2
3	224	100.0	224	5	US-10-733-646-2
4	200	89.3	200	4	US-10-612-788-10
5	187	83.5	187	4	US-10-612-788-1
6	39	17.4	39	4	US-10-612-788-8
7	39	17.4	190	4	US-10-612-788-2
8	39	17.4	224	4	US-10-612-788-12
9	37	16.5	37	4	US-10-612-788-14
10	32	14.3	32	4	US-10-612-788-5
11	32	14.3	187	4	US-10-612-788-3
12	32	14.3	224	4	US-10-612-788-13
13	26	11.6	26	4	US-10-612-788-9
14	25	11.2	25	4	US-10-612-788-6
15	24	10.7	24	4	US-10-612-788-15
16	17	7.6	17	4	US-10-612-788-7
17	13	5.8	13	4	US-10-612-788-4
18	9	4.0	870	4	US-10-437-963-172504
19	9	4.0	1077	4	US-10-437-963-172507
20	9	4.0	1408	4	US-10-437-963-172498
21	8	3.6	8	5	US-10-997-519-12
22	8	3.6	8	5	US-10-997-519-14
23	8	3.6	598	4	US-10-195-144-29
24	8	3.6	598	4	US-10-345-072-29
25	7	3.1	34	4	US-10-612-788-16
26	7	3.1	67	4	US-10-424-599-143675
27	7	3.1	73	4	US-10-424-599-279297

28	7	3.1	79	4	US-10-424-599-235015	Sequence 235015,
29	7	3.1	117	4	US-10-437-963-117184	Sequence 117184,
30	7	3.1	120	4	US-10-425-115-289504	Sequence 289504,
31	7	3.1	142	5	US-10-617-320-5033	Sequence 5033, Ap
32	7	3.1	145	4	US-10-424-599-256370	Sequence 256370,
33	7	3.1	148	4	US-10-338-083-4	Sequence 4, Appli
34	7	3.1	148	4	US-10-611-399-4	Sequence 4, Appli
35	7	3.1	148	5	US-10-794-751-4	Sequence 9, Appli
36	7	3.1	158	4	US-10-170-812-9	Sequence 4400, A
37	7	3.1	191	4	US-10-282-122A-44400	Sequence 31, Appl
38	7	3.1	204	4	US-10-468-161-31	Sequence 31, Appl
39	7	3.1	204	5	US-10-982-442A-31	Sequence 31, Appl
40	7	3.1	204	6	US-11-136-341A-31	Sequence 39, Appl
41	7	3.1	208	3	US-09-027-287-39	Sequence 39, Appl
42	7	3.1	208	3	US-09-252-656B-39	Sequence 39, Appl
43	7	3.1	208	4	US-10-375-680-39	Sequence 39, Appl
44	7	3.1	208	5	US-10-943-197-4	Sequence 4, Appli
45	7	3.1	215	4	US-10-437-963-162234	Sequence 162234,

## ALIGNMENTS

## RESULT 1

US-10-612-788-11  
; Sequence 11, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; TITLE OF INVENTION: No. US20040014947A1 Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: human  
US-10-612-788-11

Query Match	100.0%	Score 224;	DB 4;	Length 224;
Best Local Similarity	100.0%;	Pred. No. 2e-212;		
Matches 224;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPCRPLRTVPGALGAWLLGGLWAWTL	CGLCISGAVCAPRCPQAPQOWEGROVMYQSSG	60
DB	1	MPCRPLRTVPGALGAWLLGGLWAWTL	CGLCISGAVCAPRCPQAPQOWEGROVMYQSSG	60
QY	61	RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ	120	
DB	61	RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ	120	
QY	121	PWPLDIPQNSTFEDQYISGGPQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT	180	
DB	121	PWPLDIPQNSTFEDQYISGGPQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT	180	
QY	181	INYSVILSTRFFDIQILGIDKPSVFTPTSTCMAQLEKMSDCSW	224	
DB	181	INYSVILSTRFFDIQILGIDKPSVFTPTSTCMAQLEKMSDCSW	224	

## RESULT 2

US-10-733-646-2  
; Sequence 2, Application US/10733646  
; Publication No. US20040122215A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner et al.

```

; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 224; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
DB 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDEDCSW 224
DB 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDEDCSW 224

RESULT 3
US-10-733-646-2
; Sequence 2, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 224; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
DB 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDEDCSW 224
DB 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDEDCSW 224
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DB 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDEDCSW 224
DB 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDEDCSW 224

RESULT 4
US-10-612-788-10
; Sequence 10, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1e1 Human Ependymin-like Protein
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: human
US-10-612-788-10

Query Match      89.3%; Score 200; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.7e-189;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNRRALLSYDGLNQRVRLDERKA 84
DB 1 WTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNRRALLSYDGLNQRVRLDERKA 60
QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQE 144
DB 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQE 120
QY 145 QITVQWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILSTRFRFDIQLGIKDPSPV 204
DB 121 QITVQWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILSTRFRFDIQLGIKDPSPV 180
QY 205 TTPSTCQMAQLEKMSDEDCSW 224
DB 181 TTPSTCQMAQLEKMSDEDCSW 200

RESULT 5
US-10-612-788-1
; Sequence 1, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1e1 Human Ependymin-like Protein
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
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; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-612-788-1

Query Match 83.5%; Score 187; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 5.6e-176; Indels 0; Gaps 0;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 APRPCAPQWEGRQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYILL 97  
Db 1 APRPCAPQWEGRQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYILL 60  
QY 98 YKGVNFQIDQATKQCSKMTLTQWDPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 157  
Db 61 YKGVNFQIDQATKQCSKMTLTQWDPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 120  
QY 158 RSVETWIGIVTKDCYVQVQETFTINYSVILSTRFFDIQLGKDPVSFTPBSTCMAQLEK 217  
Db 121 RSVETWIGIVTKDCYVQVQETFTINYSVILSTRFFDIQLGKDPVSFTPBSTCMAQLEK 180  
QY 218 MSDEDCSW 224  
Db 181 MSDEDCSW 187

RESULT 6  
US-10-612-788-8  
; Sequence 8, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-612-788-8

Query Match 17.4%; Score 39; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.7e-30; Indels 0; Gaps 0;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106  
Db 1 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 39

RESULT 7  
US-10-612-788-2  
; Sequence 2, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02

; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Rat  
US-10-612-788-2

Query Match 17.4%; Score 39; DB 4; Length 190;  
Best Local Similarity 100.0%; Pred. No. 6.6e-30; Indels 0; Gaps 0;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106  
Db 34 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 72

RESULT 8  
US-10-612-788-12  
; Sequence 12, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Rat  
US-10-612-788-12

Query Match 17.4%; Score 39; DB 4; Length 224;  
Best Local Similarity 100.0%; Pred. No. 7.6e-30; Indels 0; Gaps 0;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106  
Db 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106

RESULT 9  
US-10-612-788-14  
; Sequence 14, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein  
; FILE REFERENCE: 2417US1P  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 37  
; TYPE: PRT  
US-10-612-788-14

; ORGANISM: human  
US-10-612-788-14

Query Match 16.5%; Score 37; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.6e-28;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGRAPLRTVPGALGNLGGIWMWTLGCLSLGAVG 37  
|||||  
DB 1 MFGRAPLRTVPGALGNLGGIWMWTLGCLSLGAVG 37  
|||||

RESULT 10  
US-10-612-788-5  
; Sequence 5, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1 Human Ependymin-like Protein  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-612-788-5

Query Match 14.3%; Score 32; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 136  
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DB 1 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 32  
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RESULT 11  
US-10-612-788-3  
; Sequence 3, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1 Human Ependymin-like Protein  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-612-788-3

Query Match 14.3%; Score 32; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 5.3e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQVRVLDERKALIPCKRLFEYILLYK 99  
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Db 31 SYDGLNQVRVLDERKALIPCKRLFEYILLYK 62

RESULT 12  
US-10-612-788-13  
; Sequence 13, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1 Human Ependymin-like Protein  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Mouse  
US-10-612-788-13

Query Match 14.3%; Score 32; DB 4; Length 224;  
Best Local Similarity 100.0%; Pred. No. 6.2e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQVRVLDERKALIPCKRLFEYILLYK 99  
|||||  
DB 68 SYDGLNQVRVLDERKALIPCKRLFEYILLYK 99  
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RESULT 13  
US-10-612-788-9  
; Sequence 9, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: ONDA, Haruo  
; TITLE OF INVENTION: No. US20040014947A1 Human Ependymin-like Protein  
; FILE REFERENCE: 2417USIP  
; CURRENT APPLICATION NUMBER: US/10/612,788  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: 09/242,890  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: PCT/JP97/03194  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-612-788-9

Query Match 11.6%; Score 26; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 8.4e-18;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQI 146  
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DB 1 PWDPLDIPQNSTFEDQYSIGGPQEQI 26  
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RESULT 14  
US-10-612-788-6  
; Sequence 6, Application US/10612788  
; Publication No. US20040014947A1  
; GENERAL INFORMATION:  
; APPLICANT: OGI, Kazuhiro



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; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 25
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-6

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Query Match      11.2%; Score 25; DB 4; Length 25;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      159 SYETWIGIYTVKDCYPVQETFTNY 183
Db      1 SYETWIGIYTVKDCYPVQETFTNY 25

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RESULT 15
US-10-612-788-15
; Sequence 15, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human
US-10-612-788-15

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Query Match      10.7%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MPGRAPLRTVPGALGAWLLGGLWA 24
Db      1 MPGRAPLRTVPGALGAWLLGGLWA 24

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Job time : 185 secs

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